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45400

**SEARCH REQUEST FORM**

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

**If more than one search is submitted, please prioritize searches in order of need.**

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval  
Reference Librarian  
Biotechnology & Chemical Library  
CM1 1E07 - 703-308-4498  
jan.delaval@uspto.gov

**STAFF USE ONLY**

## Type of Search

## Vendors and cost where applicable

Searcher: <u>Jan</u>	NA Sequence (#) <input checked="" type="checkbox"/>	STN _____
Searcher Phone #: <u>4498</u>	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>5/30/03</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>6/4/03</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: <u>20</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>K</u>	Other _____	Other (specify) _____

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**NOT AVAILABLE**

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OM nucleic - nucleic search, using sw model  
Run on: June 3, 2003, 13:38:24 ; Search time 1828.75 Seconds  
(without alignments)  
11219.411 Million cell updates/sec

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Perfect score: 705  
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Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vl:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
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- 21: em\_or:\*
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- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_sts:\*
- 28: em\_un:\*
- 29: em\_vi:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
- 35: em\_htg\_rod:\*
- 36: em\_htg\_man:\*
- 37: em\_htg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	705	100.0	705	6	AR108862	AR108862 Sequence
2	585.2	83.0	702	6	AR135374	AR135374 Sequence
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4	571.2	81.0	901	9	BC028090	BC028090 Homo sapi
5	569.8	80.8	803	9	HSIGVL022	HSIGVL022 Human rearr
6	561.8	79.7	747	9	HSIGVL031	HSIGVL031 Human rearr
7	542.8	77.0	648	9	HSIGVL031	HSIGVL031 Human rearr
8	540.2	76.6	711	6	AR108866	AR108866 Sequence
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10	534.4	75.8	826	9	AB064174	AB064174 Homo sapi
11	529.6	75.1	824	9	AB064176	AB064176 Homo sapi
12	526.4	74.7	813	9	AB064167	AB064167 Homo sapi
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14	524	74.3	725	9	HSIGVL002	HSIGVL002 Human rearr
15	522.4	74.1	890	9	BC032452	BC032452 Homo sapi
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17	520.8	73.9	904	6	AX402510	AX402510 Sequence
18	517	73.3	1154	9	BC007782	BC007782 Homo sapi
19	516.8	73.3	821	9	AB064179	AB064179 Homo sapi
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38	496	70.4	790	9	AB064233	AB064233 Homo sapi
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ALIGNMENTS

RESULT 1  
AR108862  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

AR108862  
Sequence 1 from patent US 6113898.  
AR108862  
AR108862.1 GI:12825138  
Unknown.  
Unclassified.  
1 (bases 1 to 705)  
Anderson, D.R., Brams, P., Hanna, N., Shestowsky, W.S. and Heard, C.  
Human B7.1-specific primatized antibodies and transfectomas  
expressing said antibodies  
Patent: US 6113898-A 1 05-SEP-2000;

705 bp  
DNA  
linear  
PAT 14-FEB-2001

FEATURES Location/Qualifiers  
source  
1. .705  
BASE COUNT 162 a 214 c 207 g 122 t  
ORIGIN

Query Match 100.0%; Score 705; DB 6; Length 705;  
Best Local Similarity 100.0%; Pred. No. 3e-162;  
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 GGAGGACCCGGGTGACCGTCTTAGTTCAGCCCAAGGCTGCGCTCGGTCTCTGTTTC 420  
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RESULT 2  
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LOCUS AR135374 702 bp DNA linear PAT 16-JUN-2001  
DEFINITION Sequence 5 from patent US 6136310.  
ACCESSION AR135374  
VERSION AR135374.1 GI:14476046  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 702)  
AUTHORS Hanna, N., Newman, R., Anthony, and Reff, M., Elliot.  
TITLE Recombinant anti-CD4 antibodies for human therapy  
JOURNAL Patent: US 6136310-A 5 24-OCT-2000;

FEATURES Location/Qualifiers  
source  
1. .702  
BASE COUNT 151 a 217 c 207 g 127 t  
ORIGIN

Query Match 83.0%; Score 585.2; DB 6; Length 702;  
Best Local Similarity 89.6%; Pred. No. 6.6e-133;  
Matches 629; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

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QY 124 TGTGGGGAGACAAACAGTAGAATGAATATGTCCACTGTGTACAGAGAGCCAGCGGG 183  
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QY 184 GCGCCCTTATCTGCTCATCTATGATGATGATGATGATGATGATGATGATGATGATG 243  
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QY 364 GGGACCCGGGTGACCGTCTTAGTTCAGCCCAAGGCTGCGCTCGGTCTCTGTTTCGG 423  
DB 361 GGGACCCGGGTGACCGTCTTAGTTCAGCCCAAGGCTGCGCTCGGTCTCTGTTTCGG 420

QY 424 CCGCTCTCTGAGGAGCTTCAAGCCCAACAGGCGACACTGTGTGTCTCTAAGTGACTTC 483  
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QY 484 TACCGGGAGCCCGTGAAGTGGCTTGAAGGCGATAGAGCCCGCTCAAGGCGGAGTG 543  
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QY 544 GAGACCAACACCTCCAAACAGGCAACAAAGTACGCGGCCAGCTACCTGAGC 603  
DB 541 GAGACCAACACCTCCAAACAGGCAACAAAGTACGCGGCCAGCTACCTGAGC 600

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QY 664 AGCACCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 705  
DB 661 AGCACCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 702

RESULT 3  
AB064177  
LOCUS AB064177 820 bp mRNA linear PRI 02-JUL-2002  
DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ region, partial cds, clone:137.  
ACCESSION AB064177  
VERSION AB064177.1 GI:21669560  
KEYWORDS Homo sapiens cDNA to mRNA, clone lib:AIMS4 clone:137.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 702)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
JOURNAL Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,



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Best Local Similarity 90.8%; Pred. No. 1.8e-129;
Matches 632; Conservative 0; Mismatches 58; Indels 6; Gaps 2;
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QY 71 TGACTCAGCACCCCTCGGTGTCAGTGTCCAGGACAGACGGCCAGGATCACCTGTGGGG 130
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QY 131 GAGACACAGTAGAATATATGTCCATGTTACAGGACAGACGCGCGGGCCCTTA 190
DB 167 GAAACCAACATTGGAAGTAAAGTGTGCACTGGTACCAGCAGAGACGCGGCGCCCTG 226
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DB 647 CGCCTGAGCAGTGGAGTCCCAAGAGTACAGTGTCCAGGTTCAGCATGAAGGGAGCA 706
QY 668 CCGTGGAGAGACAGTGGCCCTACAGATGTTTCAT 703
DB 707 CCGTGGAGAGACAGTGGCCCTACAGATGTTTCAT 742
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DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION X57812
VERSION X57812.1 GI:33723
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 803)

Direct SubMISSION

Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany

2 (bases 347 to 393)

Combiato.G. and Klobeck,H.G.

V lambda and J lambda-C lambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism

Eur. J. Immunol. 21 (6), 1513-1522 (1991)

91257162

1904362

for overlapping sequences see: X51754-55; J00252-54; M15641-42.

Location/Qualifiers

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/isolate="individual ML"

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BASE COUNT

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Best Local Similarity 92.8%; Pred. No. 3.9e-129;

Matches 596; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 62 CCTATGAACCTGACTCAGCCACCTCGGTGTCTAGTGTCCCGCAGCAGACGCGGATCA 121

DB 68 CCTATGTGCTGACTCAGCCACCTCGGTGTCTAGTGTCCCGCAGCAGGCGGCGGATTA 127

QY 122 CTTGTGGGGGAGACACAGTAGAATATGTCCATGTTACCTGAGCAGAGCCGCGC 181

DB 128 CTTGTGGGGGAAATCAACATTGCAAGTAAAGTGTCTGTTACCTGAGCAGAGCCGCGC 187

QY 182 GGGCCCTTACTCTGCTCATCTATGATGATGACGCGGCCCTCAGGATCCCTGAGCGAT 241

DB 188 AGGCCCTTGTGCTGCTCTATGATGATGACGCGGCCCTCAGGATCCCTGAGCGAT 247



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QY 242 TCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGTCGAGCGCGGG 301
Db 248 TCTCTGGCTCCAACTTGGGAACACCGCCACCTGAACTCAGTAGGGTCGAAGCGCGGG 307
QY 302 ATGAGGCTGACTATTACTGTGAGGTGGGACAGGGCTAGTGATCATCGGTCCTCGGAG 361
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QY 542 TGGAGACCAACACACCTTCCAAACAAGCAACAAGTACGGCGGCGAGCTACTCTGA 601
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QY 602 GCCTGACGCTGAGCAGTGAAGTCCCAAGAAGCTACAGTCCGAGGTCAAGCATGAAG 661
Db 608 GCCTGACGCTGAGCAGTGAAGTCCCAAGAAGCTACAGTCCGAGGTCAAGCATGAAG 667
QY 662 GGAGCACCGTGGAGAGACAGTGGCCCTACAGATGTTTCAT 703
Db 668 GGAGCACCGTGGAGAGACAGTGGCCCTACAGATGTTTCAT 709
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## RESULT 6

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HSIGVL031
LOCUS 747 bp mRNA linear PRI 04-NOV-1994
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION X57821
VERSION X57821.1 GI:33741
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Klobeck.H.G.
Direct Submission
Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische
Chemie, Physiologische Biochemie und Zellbiologie der Universitaet
Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany
2 (bases 340 to 386)
Combratio,G. and Klobeck,H.G.
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
Eur. J. Immunol. 21 (6), 1513-1522 (1991)
91257162
1904362
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.
FEATURES
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63..384
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347..384
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/note="constant region"
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Best Local Similarity 93.1%; Pred. No. 3.6e-127;
Matches 598; Conservative 0; Mismatches 41; Indels 3; Gaps 1;
QY 62 CCTATGAACCTGACTCAGCCACCTCGGTGTCAAGTCCCGGACAGAGCGCCAGGATCA 121
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QY 122 CTTGTGGGGGAGACAACAGTGAATAATGATGTCCACTGGTACACAGAGAGAGCCAGCGC 181
Db 124 CTTGTGGGGGAAATACATTTGAAGTGTGCATCTGGTACACAGAGAGAGCCAGGCC 183
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QY 362 GAGGACCCCGGTGACCGTCTTAGGTGACGCCAAGGCTGCCCTCGGTCACTCTGTTC 421
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QY 662 GGAGCACCGTGGAGAGACAGTGGCCCTACAGATGTTTCAT 703
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 QY 415 CTGTTCCCGCCCTCTCTCAGAGCTTCAAGCCCAACAAAGGCCACACTGGTGTCTCATA 474  
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 ACCESSION AB064230  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE

JOURNAL  
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 AUTHORS  
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 JOURNAL

COMMENT  
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BASE COUNT 183 a 238 c 223 g 146 t  
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Query Match 76.3%; Score 538; DB 9; Length 790;  
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 Matches 591; Conservative 0; Mismatches 45; Indels 6; Gaps 1;

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QY 130 GCGAGACACAGTAGAATAATATGTCACCTGGTACCAGCAGACGCGCGGGCCCT 199  
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QY 190 ATACTGGTCACTATGATGATAGTGAACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGC 249  
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Db 196 GTGCTGGTCACTATAGGATAGCAACCGGCCCTCTGGGATCCCTGAGCGATTCTCTGGC 255  
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QY 250 TCCAAATCAGGAACACCGCCACCTGACCATCAACGGGTGAGGCGCGGGATGAGGCT 309  
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QY 430 TCTGAGGAGCTTCAAGCCCAAGGCCACACTGGTGTGTCTCATAGTGACTTCTACCCG 489  
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Db 430 TCTGAGGAGCTTCAAGCCCAAGGCCACACTGGTGTGTCTCATAGTGACTTCTACCCG 489  
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QY 490 GAGCGCTGACAGTGGCTGGAGCCAGTACAGCCCGCTCAAGCGGGAGTGGAGACC 549  
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Db 490 GAGCGCTGACAGTGGCTGGAGCCAGTACAGCCCGCTCAAGCGGGAGTGGAGACC 549  
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Db 610 CTGAGCAGTGGAAAGTCCCAAGAGCTACAGCTGCCAGGTCAAGCATGAAGGAGCACC 669  
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RESULT 10  
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 DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ region, partial cds, clone:L34.  
 ACCESSION AB064174  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE

**TITLE**  
Miura, K. and Kurosawa, Y.  
Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics

**JOURNAL**  
Unpublished  
2 (bases 1 to 826)

**REFERENCE**  
Kurosawa, Y.  
Direct Submission  
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University, Kutsukake-cho, Toyooka 470-1192, Japan  
(E-mail: kurosawa@fujita-hu.ac.jp, Tel: 81-562-93-9387)  
Please visit our web site  
URL: http://www.fujita-hu.ac.jp/immunity/.

**COMMENT**  
Location/Qualifiers

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BASE COUNT 172 a 244 c 246 g 164 t  
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Best Local Similarity 89.7%; Pred. No. 1.8e-120;  
Matches 574; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

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**Db** 128 CTTGTGGGGAGAGACGAGTTGGAGGTAAGTGTTCACCTGATATCAGCAAGCCAGGCGC 187  
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**QY** 182 GGGCCCTATCTGTCATCTATGATAGTACGCGGCCCTCAGGATCCCTGAGCGAT 241  
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**QY** 242 TCTCTGGCTCCAATCAGGGAACACCGCACCTGACCATCAACGGGTGCGGCGCGGG 301  
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**RESULT 11**  
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LOCUS  
DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ region, partial cds, clone:L36.  
ACCESSION AB064176  
VERSION AB064176.1 GI:21669558  
KEYWORDS  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.  
TITLE Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 824)  
AUTHORS Kurosawa, Y.  
TITLE Direct Submission  
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University, Kutsukake-cho, Toyooka 470-1192, Japan  
(E-mail: kurosawa@fujita-hu.ac.jp, Tel: 81-562-93-9387)  
Please visit our web site  
URL: http://www.fujita-hu.ac.jp/immunity/.

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BASE COUNT 170 a 248 c 242 g 164 t  
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Query Match 75.1%; Score 529.6; DB 9; Length 824;  
 Best Local Similarity 89.2%; Pred. No. 2.7e-119;  
 Matches 571; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 62 CCTATGAAGTCACTCAGCCACCTCGGTGTCCCGCAGACAGCGCCAGGATCA 121  
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QY 122 CCTGTGGGGAGACAACAGTAGAATAATATGTCTCACTGGTACAGCAAGCCAGCGC 181  
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QY 182 GGGCCCTATCTAGTCTATCATATGATAGTACCGGCCCTCAGGATCCCTGAGGCAT 241  
 DB 188 AGGCCCTCTGCTGGTGTCTTTGATACCGGACCGGCCCTCAGGCATCCCTGACCGAT 247

QY 242 TCTCTGGCTCCAATCAGGGAACAACGCCACCTGACCATCAACGGGGTCCAGCGCGGG 301  
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QY 362 GAGGACCCGGGTGACCGTCTTAGTTCAGCCCAAGGTGCGCCCTCGGTCACTCTGTTC 421  
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QY 422 CGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCACACTGGTGTCTCATAGTCACT 481  
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QY 602 GCCTGACGCTGAGCAGTGAAGTCCACAGAGCTACAGTCCCGGTCACCATGAG 661  
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 DB 668 GGAGCACCGGTGGAGAGACAGTGGCCCTTACAGAAATGTTTC 707

RESULT 12  
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 LOCUS  
 DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ  
 region, partial cds, clone:L27.  
 ACCESSION AB064167  
 VERSION AB064167.1 GI:21669540  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens cDNA to mRNA, clone\_lib:AIMS4 clone:L27.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 AUTHORS Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,  
 Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,  
 Miura, K. and Kurosawa, Y.  
 TITLE Construction and characterization of antibody libraries: isolation  
 of therapeutic human antibodies and application to functional  
 genomics  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 813)  
 AUTHORS Kurosawa, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for

Comprehensive Medical Science, Fujita Health University;  
 Kutsukake-cho, Toyooka 470-1192, Japan  
 (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)  
 please visit our web site  
 URL:http://www.fujita-hu.ac.jp/immunity/.

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 Matches 569; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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 DB 128 CTTGTCTCTGAGATGCAATTTGCCAAAGCAATATGCTTATTGGTACCAGCAAGCCAGGCC 187

QY 182 GGGCCCTCTACTGTGTCACTATGATGATGACCGGCCCTCAGGATCCCTGAGGCAT 241  
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QY 242 TCTCTGGCTCCAATCAGGGAACAACGCCACCTGACCATCAACGGGGTCCAGCGCGGG 301  
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QY 302 ATGAGGCTCACTATTACTGTGAGTGGGACAGGCTAGTATCATCCGGTCTTCGGAG 361  
 DB 308 ACAGGCTCACTATTACTGTCAATCAGCAGCAGCAGTGTGTACTTATGTGTATTCGGCG 367

QY 362 GAGGACCCGGGTGACCGTCTTAGTGTGACCCCAAGGTGCGCCCTCGGTCACTCTGTTC 421  
 DB 368 GAGGACCAAGCTGACCGTCTTAGTGTGACCCCAAGGTGCGCCCTCGGTCACTCTGTTC 427

QY 422 CGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCACACTGGTGTCTCATAGTCACT 481  
 DB 428 CGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCACACTGGTGTCTCATAGTCACT 487

QY 482 TCTACCCGGGAGCGGTGACAGTGGCCCTCAAGCAACAGGCTCAGCAGCCCGGAG 541  
 DB 488 TCTACCCGGGAGCGGTGACAGTGGCCCTCAAGCAACAGGCTCAGCAGCCCGGAG 547

QY 542 TGAGACCAACACACCTTCCAAACAAAGCAACAAAGTACGCGGCGAGTCACTCTGA 601  
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QY 602 GCCTGACGCTGAGCAGTGAAGTCCACAGAGCTACAGTCCCGGTCACCATGAG 661  
 DB 608 GCCTGACGCTGAGCAGTGAAGTCCACAGAGCTACAGTCCCGGTCACCATGAG 667

Db 608 GCCTGACGCTGAGCGATGGAAGTCCACAGAGAGCTACAGCTGCCAGGTCAACGATGAAG 667  
 QY 662 GGAGCACCCTGGGAGAGACAGAGTGGCCCTACAGATGTTTC 701  
 Db 668 GGAGCACCCTGGGAGAGACAGAGTGGCCCTACAGATGTTTC 707

RESULT 13  
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 LOCUS Homo sapiens, clone MGC:39283 IMAGE:4856249, mRNA, complete cds.  
 DEFINITION BC022823  
 ACCESSION BC022823.1 GI:18606083  
 VERSION MGC.  
 KEYWORDS Homo sapiens.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Strausberg, R.  
 Direct Submission  
 Submitted (04-FEB-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-rc@mail.nih.gov](mailto:cgapbs-rc@mail.nih.gov)  
 Tissue Procurement: Louis Staudt  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Genome Sequence Centre,  
 BC Cancer Agency, Vancouver, BC, Canada  
 info@bcgsc.bc.ca

REMARK  
 COMMENT  
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,  
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
 Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo  
 Sen Lee, Victor Ling, Martin Mathewson, Candice McLeavy, Steven  
 Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline  
 Schein, Duane Smalus, Michael Smith, Lorraine Spence, Jeff Strott,  
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,  
 George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 42 Row: g Column: 21  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: Hexamer frequency ORF  
 analysis, Genomescan gene prediction, Similarity but not identity  
 to protein.

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 VERSION Ig lambda light chain; immunoglobulin.  
 KEYWORDS Homo sapiens.  
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 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Klobeck, H.G.  
 Direct Submission  
 Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische  
 Chemie, Physikalische Biochemie und Zellbiologie der Universitaet  
 Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany  
 REFERENCE 2 (bases 355 to 401)  
 AUTHORS Combratio, G. and Klobeck, H.G.  
 TITLE V lambda and J lambda-C lambda gene segments of the human  
 immunoglobulin lambda light chain locus are separated by 14 kb and  
 rearrange by a deletion mechanism  
 Eur. J. Immunol. 21 (6), 1513-1522 (1991)  
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 PUBMED  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 14:15:24 ; Search time 961.424 Seconds  
(without alignments)  
11875.950 Million cell updates/sec

Title: US-09-576-424-1  
Perfect score: 705  
Sequence: 1 atgagggtcccgctcagct.....ccctacagaatgttcataga 705

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits.satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hcti:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hcti:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pin:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES			
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2	555.6	78.8	BQ709526
3	555.2	78.8	BQ711683
4	552	78.3	BQ757730
5	552	78.3	BQ707953
6	551.2	78.2	BQ708246

7	548.8	77.8	920	14	BQ711280	BQ712280	AGENCOURT
8	547.2	77.6	925	14	BQ710672	BQ710672	AGENCOURT
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	10	545.8	77.4	908	14	BQ884067	AGENCOURT
	11	545.6	77.4	754	13	B1907909	AGENCOURT
	12	545.2	77.3	924	12	BQ756256	AGENCOURT
	13	545	77.3	1086	14	BQ924274	AGENCOURT
	14	544.4	77.2	917	14	BQ711587	AGENCOURT
	15	542.4	76.9	949	14	BQ709509	AGENCOURT
	16	541.6	76.8	1018	14	BQ914338	AGENCOURT
	17	540.8	76.7	947	14	BQ709579	AGENCOURT
	18	540.4	76.7	789	13	B1765865	AGENCOURT
	19	537	76.2	742	13	B1906298	AGENCOURT
	20	533.6	75.7	874	12	BQ755301	AGENCOURT
	21	531	75.3	837	12	BQ754193	AGENCOURT
	22	530.2	75.2	731	10	AV649126	AGENCOURT
	23	529	75.0	803	12	BQ758687	AGENCOURT
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	29	520.2	73.8	871	12	BQ758687	AGENCOURT
	30	517.2	73.4	1005	12	BQ758687	AGENCOURT
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c	33	513.8	72.9	868	12	BQ758687	AGENCOURT
	34	512.8	72.7	923	14	BQ758687	AGENCOURT
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	36	508.4	72.1	782	13	BQ758687	AGENCOURT
	37	508.2	72.1	801	13	BQ758687	AGENCOURT
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	39	501.8	71.2	688	12	BQ758687	AGENCOURT
c	40	499.8	70.9	722	14	BQ758687	AGENCOURT
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ALIGNMENTS

RESULT 1  
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LOCUS BQ711447 952 bp mRNA linear EST 16-JUL-2002  
DEFINITION AGENCOURT\_8353624 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6279618  
5', mRNA sequence.  
ACCESSION BQ711447  
VERSION BQ711447.1 GI:21850346  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 952)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)  
Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
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High quality sequence stop: 584.  
Location/Qualifiers  
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QY 488 CGGAGCCGTGACAGTGGGCTGGAAGGAGATAGAGCCCGTCAAGGCGGAGTGGAGA 547  
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## RESULT 3

BQ711683  
 LOCUS AGENCOURT\_8485100 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6301194  
 DEFINITION 5', mRNA sequence.

ACCESSION BQ711683  
 VERSION BQ711683.1  
 KEYWORDS GI:21850582  
 SOURCE EST.

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 931)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)

## AUTHORS

Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)

Tissue Procurement: Dr. Mark Watson  
 cDNA Library Preparation: Rubin Laboratory  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

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 High quality sequence stop: 549.

## FEATURES

Location/Qualifiers  
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/lab\_host="DH10B (phage-resistant)"

/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

BASE COUNT 222 a 286 c 248 g 171 t 4 others

## ORIGIN

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 DEFINITION mRNA sequence.

ACCESSION BQ757730  
 VERSION BQ757730.1  
 KEYWORDS GI:14068383  
 SOURCE EST.

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 796)  
 NIH-MGC <http://mgs.nci.nih.gov/>.

## AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)

## TITLE

Contact: Robert Strausberg, Ph.D.

Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

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High quality sequence stop: 795.

## FEATURES

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/db\_xref="taxon:9606"



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DEFINITION AGENCOURT_8495393 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301917
5', mRNA sequence.
B0708246
VERSION B0708246.1 GI:21847145
KEYWORDS EST.
SOURCE human.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE 1 (bases 1 to 921)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

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CDNA Library Preparation: Rubin Laboratory
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC2518 row: i column: 22
High quality sequence stop: 628.
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/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GACACAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC Library."

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source

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Query Match 78.2%; Score 551.2; DB 14; Length 921;
Best Local Similarity 92.1%; Pred. No. 4.2e-132;
Matches 604; Conservative 0; Mismatches 48; Indels 4; Gaps 2;

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QY 52 GCACGATGTCCTATGAACCTGACTGACCCCTCGGTGTGAGTGTCCCGACAGACG 111
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Db 3 GCACGAGGCTCTATGTGCTGACTGACCCACCTCGGTGTGAGTGTCCCGACAGACG 62
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QY 112 GCACGATCACCT-GTGGGGGACACACAGTGAATGATGTCCACTGTGTCACGCA 170
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Db 63 GCACGATTCCTGTGGTGGGGGAAACAACTTACAGGTAAACAGTGTGCTGTGTCACGCA 122
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QY 171 GAAGCCAGCGCGGGCCCCCTTATCTGGTCACTCTATGATGATGATGATGATGATGATGATGAT 230
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QY 231 CCTCAGCGGATTTCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGT 290
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Db 183 CCTCAGCGGATTTCTCTGGCTCCAACTTGGGAACACCGCCACCTGACCATCAACGGGGT 242
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QY 291 CGAGGCCGCGGGATGAGGCTGACTATTACTGTGAGGTGTGGGACAGGGCTAGTATCATCC 350
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Db 243 CGAAGCCGCGGGATGAGGCGGACTATTACTGTGAGGTGTGGGATACTACTGATGATCATCC 302
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QY 351 ---GGTCTTCGAGGAGGAGCCCGGGTGACCGTCTCTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 407
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Db 303 TGTGGTATTTCGGCGGAGGAGCAAGCTGACCGTCTCTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 362
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QY 408 GGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGTGTGTG 467
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Db 363 GGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGTGTGTG 422
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QY 468 TCTCATAAGTGAATTTCTACCCGGGAGCCGTGACAGTGGCTTGAAGGCAGATAGCAGCCC 527
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Db 423 TCTCATAAGTGAATTTCTACCCGGGAGCCGTGACAGTGGCTTGAAGGCAGATAGCAGCCC 482
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QY 528 COTCAAGCGGAGTGGAGACCAACACACCTTCCAAACAAAGCAACAAAGTACCGGC 587
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Db 483 CGTCAAGCGGAGTGGAGACCAACACACCTTCCAAACAAAGCAACAAAGTACCGGC 542
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QY 588 CAGCAGCTACTCTGAGCCTGAGCCCTGAGCGAGTGGAGTCCACAGAGCTAGCTGCCA 647
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QY 648 GGTCAAGCATGAAGGAGCAGCCGTGGAGAGACAGTGGCCCTCAGAGATGTTTCAT 703
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B0712280 920 bp mRNA linear EST 16-JUL-2002
AGENCOURT_8353529 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279636
5', mRNA sequence.
B0712280
VERSION B0712280.1 GI:21851179
KEYWORDS EST.
SOURCE human.
ORGANISM

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE 1 (bases 1 to 920)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

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Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC2469 row: i column: 13
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Location/Qualifiers
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/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:

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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GACACAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC Library."

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FEATURES
source

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EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

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BASE COUNT      216 a      281 c      246 g      176 t      1 others
ORIGIN
Query Match      77.8%; Score 548.8; DB 14; Length 920;
Best Local Similarity 88.8%; Pred. No. 1.8e-131;
Matches 618; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 11 CCCTCAGCTCCCTGGGCTCCTGCTCTGGCTCCAGGTGACGATGCTATGAAC 70
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 37 CCGTCTCTCTCTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 93
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 71 TGACTCAGCCACCTCGGTGTCAGTGTCCAGGACAGACGGCCAGGATCACCTGTGGG 130
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 94 TGACTCAGACACCTCGGTGTCAGTGTCCAGGACAGACGGCCAGGATTTCTGTGGG 153
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 131 GAGACACAGTGAATGATATGTCCTGCTGTCAGTGTCCAGGACAGACGGCCAGG 190
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QY 154 GAAACAACTTGAAGAAAAGTGTTCCTGTTACCGACAGACGGCCAGGCCCCCTC 213
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 311 ACTATTACTGTCTAGTGTGGGACAGGCTAGTATCATTC---GGTCTCGGAGGGA 367
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QY 334 ACTATTACTGTCTAGTGTGGGATGATGTTGATCTGTTCTGTGTGTTTCTGGTGGGA 393
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 368 CCGGGTGACCGTCTAGGTTCAGCCCAAGGCTCCCGCTCGGTCACTCTGTTCCCGCCCT 427
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 394 CCAAGCTGACCGTCTAGGTTCAGCCCAAGGCTCCCGCTCGGTCACTCTGTTCCCGCCCT 453
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 428 CTTCTGAGGAGTTCAGGCAACAGGCCACACTGTGTGTCTCTATAAGTGACTTCTACC 487
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 454 CTTCTGAGGAGTTCAGGCAACAGGCCACACTGTGTGTCTCTATAAGTGACTTCTACC 513
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 488 CGGAGCCGTGACAGTGGCTTGAAGGCAGATAGCAGCCCCCTCAAGCGGGAGTGGAGA 547
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 514 CGGAGCCGTGACAGTGGCTTGAAGGCAGATAGCAGCCCCCTCAAGCGGGAGTGGAGA 573
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 574 CCACCAACCTCCAAACAAAGCAACAAAGTACCGGCCAGCAGCTACTCTGAGCTGA 633
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QY 608 CGCTGAGCAGTGGAGTCCCAAGAGCTTACAGTTCAGGTCACGCATGAAGGGAGCA 667
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QY 634 CGCTGAGCAGTGGAGTCCCAAGAGCTTACAGTTCAGGTCACGCATGAAGGGAGCA 693
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 668 CCGTGAGAGACAGTGGCCCCCTACAGATGTTTCAT 703
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QY 694 CCGTGAGAGAACAGTGGCCCCCTACAGATGTTTCAT 729
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RESULT 8
LOCUS BQ710672
DEFINITION BQ710672 925 bp mRNA linear EST 16-JUL-2002
AGENCY AGENCOURT_848950 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301041
5', mRNA sequence.
ACCESSION BQ710672
VERSION BQ710672.1
KEYWORDS EST.
SOURCE BQ710672.1 GI:21849571
ORGANISM human.
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 925)  
NIH-MGC <http://mhc.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Dr. Mark Watson  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LCM2516 row: e column: 10  
High quality sequence stop: 661.  
Location/Qualifiers  
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BASE COUNT      214 a      293 c      239 g      170 t      9 others
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Query Match      77.6%; Score 547.2; DB 14; Length 925;
Best Local Similarity 88.6%; Pred. No. 4.6e-131;
Matches 617; Conservative 0; Mismatches 73; Indels 6; Gaps 2;

QY 11 CCGCTCAGCTCTCTGGGCTCCTGCTCTGCTCCAGGTGACGATGCTATGAAC 70
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 38 CCGTCTCTCTCTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 94
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 71 TGACTCAGCCACCTCGGTGTCAGTGTCCAGGACAGACGGCCAGGATCACCTGTGGG 130
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 95 TGACTCAGCCACCTCGGTGTCAGTGTCCAGGACAGACGGCCAGGATTTCTGTGGG 154
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 131 GAGACAAAGTGAATGATGTCCTGTCAGTGTCCAGGACAGACGGCCAGGCCCCCTA 190
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 155 GAAACAAATTTGGAAGTAGAAGTGTGCTGTTACCGACAGACTTCAGGCCAGGCCCTG 214
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 191 TACTGTCTATCTATGATGATGACCGCCCTCAGGATCCCTGAGCGATTTCTTGGCT 250
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 215 TCTGTGTCTCTATGATGATGACCGGCCCTCGGGGATCCCTGAGCGATTTCTTGGCT 274
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DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 368 CCGGGTGACCGTCTCTAGGTGACCGCCCTCAGGATCCCTGAGCGATTTCTTGGCT 427
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 395 CCAAGCTGACCGTCTCTAGTTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCT 454
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QY 428 CTTCTGAGGAGTTCAGGCAACAGGCCACACTGTGTGTCTCTATAAGTGACTTCTACC 487
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 455 CTTCTGAGGAGTTCAGGCAACAGGCCACACTGTGTGTCTCTATAAGTGACTTCTACC 514
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 488 CGGAGCCGTGACAGTGGCTTGAAGGCAGATAGACGCCCTCAAGCGGGAGTGGAGA 547
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db      515  CGGAGCCGTGACAGTGGCTGGAAGCGAGATAGACGCCCGTCAAGGGCGGAGTGGAGA 574
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Db      575  CCACCAACACCTCCAAACAAAGCAACAAAGTACCGCGCCAGCAGCTATCTGAGCCTGA 634
QY      608  CCCTGAGCAGTGGAGTCCCAAGAGCTACAGCTGCGCAGCTCAGCAGTGAAGGAGCA 667
Db      635  CGCTGAGCAGTGGAGTCCCAAGAGCTACAGCTGCGCAGCTCAGCAGTGAAGGAGCA 694
QY      668  CGCTGAGAGAGCAGTGGCGCCCTACAGAAATGTTTCAT 703
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LOCUS      602723726T1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:4849878 3',
DEFINITION mRNA sequence.
ACCESSION BG746204
VERSION    BG746204.1 GI:14056857
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 832)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Prepared by: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1690 row: d column: 07
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                EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                into EcoRI/XhoI sites using the following 5' adaptor:
                GGCACGAG(G). Library constructed by Ling Hong in the
                laboratory of Gerald M. Rubin (University of California,
                Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                Superscript II RT (Life Technologies). Note: this is a
                NIH MGC Library."
BASE COUNT 152 a 232 c 263 g 185 t
ORIGIN

Query Match 77.4%; Score 546; DB 12; Length 832;
Best Local Similarity 92.4%; Pred. No. 9.1e-131;
Matches 597; Conservative 0; Mismatches 45; Indels 4; Gaps 2;

QY      62  CCTATGAATGACTAGCACCCTCGTGTCACTGTCAGTGTCCCGGAGGAGAC-GGCCAGGATC 120
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QY      121  ACCTGTGGGGGAGACAAACAGTAGAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCG 180
Db      679  ACCTGTGGGGGTCCTCCAAACATTGGAACTTACAGTGTGCATGTGTACCAGCAGAAGTCAGGC 620
QY      181  CGGGCCCCCTATACTGTGTCATCTATGATGATAGTAGTGACCGGCCCTCAGGGATCCCTGAGCGA 240

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Db      619  CAGGCCCCCTGTCTGTCTATGATGATAGCGACCGGCCCTCAGGGATCCCTGAGCGA 560
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QY      301  GATGAGGCTGACTATTACTGTGAGGTGGGACAGGGCTAGTGATCATCCGGT---CTTC 357
Db      499  GATGAGGCGCGACTATTACTGTGAGGTGTCGAGTAGTGGTAGTATCATCTGTGCAATTC 440
QY      358  GGAGGAGGAGACCGGGGTGACCGCTAGTGTAGTACGCCCAAGGCTGCCCTCGTCACTCTG 417
Db      439  GCGGAGGAGGACCAAACTGACCGCTTAGTGTAGTCCGAGGCTGCCCTCGTCACTCTG 380
QY      418  TTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAAAGGCCACACTGTGTGTCTCATAAGT 477
Db      379  TTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAAAGGCCACACTGTGTGTCTCATAAGT 320
QY      478  GACTTCTTACCCCGGAGCCGTGACAGTGGCTCGAAGGCGAGTAGCAGCCCGCTCAAGGCG 537
Db      319  GACTTCTTACCCCGGAGCCGTGACAGTGGCTCGAAGGCGAGTAGCAGCCCGCTCAAGGCG 260
QY      538  GAGTGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACCGGCCGAGCAGCTAC 597
Db      259  GGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACCGGCCGAGCAGCTAT 200
QY      598  CTGAGCTGACCCCTGAGCAGTGGAGTCCCAACAGAGCTACAGTGCAGGTCACGCGCAT 657
Db      199  CTGAGCTGACCCCTGAGCAGTGGAGTCCCAACAGAGCTACAGTGCAGGTCACGCGCAT 140
QY      658  GAAGGAGCAGCCTGGAGAGACAGTGGCCCTTACAGAAATGTTTCAT 703
Db      139  GAAGGAGCAGCCTGGAGAGACAGTGGCCCTTACAGAAATGTTTCAT 94

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AGENCOURT_8616484 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302471
5', mRNA sequence.
BQ884067
VERSION      BQ884067.1 GI:22276075
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 908)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Prepared by: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2519 row: p column: 24
            High quality sequence stop: 687.
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                EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                into EcoRI/XhoI sites using the following 5' adaptor:
                GGCACGAG(G). Library constructed by Ling Hong in the
                laboratory of Gerald M. Rubin (University of California,
                Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                Superscript II RT (Life Technologies). Note: this is a
                NIH MGC Library."
BASE COUNT 152 a 232 c 263 g 185 t
ORIGIN

FEATURES
            source

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Db 575 CACCACACCTCCAAACAAAGCAACAAGTACGGCCAGCAGCTACTGAGCTGAC 634  
 QY 609 GCTGTAGAGTGAAGTCCACAGAGCTACA-GTGTCCAGGTACGCATGAAGGAGCA 667  
 Db 635 GCTGTAGAGTGAAGTCCACAAAGCTACAGGTGCGAGGTACGCATGAAGGAGCA 694  
 QY 668 CCGTGGAGAGACAGTGGCCCTACAGATGTTTAT 703  
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 SOURCE human.  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 924)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM1700 row: 9 column: 18  
 High quality sequence stop: 786.  
 Location/Qualifiers  
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 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
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 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC library."  
 226 a 272 c 257 g 169 t

FEATURES  
source

BASE COUNT 226 a 272 c 257 g 169 t  
 ORIGIN  
 Query Match 77.3%; Score 545.2; DB 12; Length 924;  
 Best Local Similarity 92.7%; Pred. No. 1.5e-130;  
 Matches 595; Conservative 0; Mismatches 43; Indels 4; Gaps 2;  
 QY 62 CCTATGAATGACTCAGCACACCTCGGTGTCAAGTGTCCCGCAGCAGAGCGGCAGGATCA 121  
 Db 14 CCTATGTGTGACTCAGCACACCTCGGTGTCAAGTGTCCCGCAGCAGAGCGGCAGGATTA 73  
 QY 122 CTTGTGGGGAGACAAACAGTAGAATATGATGTCCATGTGTGACACGAGAGCCAGCCG 181  
 Db 74 CTTGTGGGGAGACAAACATTGGAAGTAAAGTGTGCTGTTATCAGCAGAGAGCCAGGCC 133  
 QY 182 GGGCCCCCTATCTGTCATCTATGATAGTACCGGCCCTCAGGGATCCCTGACCGAT 241  
 Db 134 AGGCCCCCTGTGTGGTGTGCTTATGAAGATAGTAGACCGGCCCTCAGGGATCCCTGACCGAT 193

QY 242 TCTTGGGTCCAAATCAGGGAACACCGCCACCCCTGACCATCAACCGGGTTCGAGGCGGG 301  
 Db 194 TCTTGGGTCCAACTCTGTGGAAACACGGCCACCCCTGACCATCAGCAGGGTTCGAAGCGGG 253  
 QY 302 ATGAGGCTGACTATTACTGTGAGGTGTGGGACAGGGCTAGTATCATCCGCTCTTCGGAG 361  
 Db 254 ATGAGGCGGACTATTACTGTGAGGTGTGGGATAGAAGTAGTG---ATGTAGTATTTCGGCG 310  
 QY 362 GAGGACCCGGGTGACCCGTCTCTAGGTACAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC 421  
 Db 311 GAGGACCAAGCTGACCGTCTGTAGTACAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC 370  
 QY 422 GCGCTCTCTGTAGAGGCTTCAAGCAACAAGCCACACTGTGTGTCTCTATAAGTGACT 481  
 Db 371 GCGCTCTCTGTAGAGGCTTCAAGCAACAAGCCACACTGTGTGTCTCTATAAGTGACT 430  
 QY 482 TCTACCCGGGAGCCGTGACAGTGGCTCGAAGGCGAGTAGCAGCCCGTCAAGGCGGGAG 541  
 Db 431 TCTACCCGGGAGCCGTGACAGTGGCTCGAAGGCGAGTAGCAGCCCGTCAAGGCGGGAG 490  
 QY 542 TGGAGACCAACACACCCCTCCAAACAAAGCAACAAGTACGCGGCCAGCAGCTACCTGA 601  
 Db 491 TGGAGACCAACACACCCCTCCAAACAAAGCAACAAGTACGCGGCCAGCAGCTATCTGA 550  
 QY 602 GCGTACCGCTGAGCAGTGGAGTCCCAAGAGTACAGTTCGCGGTCAGGTCACGCATGAAG 661  
 Db 551 GCGTACCGCTGAGCAGTGGAGTCCCAAGAGTACAGTTCGCGGTCAGGTCACGCATGAAG 610  
 QY 662 GGAGCACCGTGGAGAGACAGTGGCCCTCAGCAAGATGTTTAT 703  
 Db 611 GGAGCACCGTGGAGAGACAGTGGCCCTCAGCAAGATGTTTAT 651

## RESULT 13

LOCUS BM924274 1086 bp mRNA linear EST 12-MAR-2002  
 DEFINITION AGENCOURT\_6630576 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5760519  
 5', mRNA sequence.  
 ACCESSION BM924274  
 VERSION BM924274.1 GI:19374641  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1086)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM12807 row: k column: 16  
 High quality sequence stop: 710.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5760519"  
 /clone\_lib="NIH\_MGC\_116"  
 /lab\_host="DH10B"  
 /note="Organ: pooled colon, kidney, stomach; Vector:  
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
 source anonymous pool of 3 colons, age 26 yo male, 49 yo  
 female, 71 yo male colon, 46 yo male kidney, and pool of 2  
 stomachs, 62 yo male and 70 yo female. Library is

FEATURES  
source

QY 62 CCTATGAATGACTCAGCACACCTCGGTGTCAAGTGTCCCGCAGCAGAGCGGCAGGATCA 121  
 Db 14 CCTATGTGTGACTCAGCACACCTCGGTGTCAAGTGTCCCGCAGCAGAGCGGCAGGATTA 73  
 QY 122 CTTGTGGGGAGACAAACAGTAGAATATGATGTCCATGTGTGACACGAGAGCCAGCCG 181  
 Db 74 CTTGTGGGGAGACAAACATTGGAAGTAAAGTGTGCTGTTATCAGCAGAGAGCCAGGCC 133  
 QY 182 GGGCCCCCTATCTGTCATCTATGATAGTACCGGCCCTCAGGGATCCCTGACCGAT 241  
 Db 134 AGGCCCCCTGTGTGGTGTGCTTATGAAGATAGTAGACCGGCCCTCAGGGATCCCTGACCGAT 193

oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library."

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BASE COUNT      255 a   355 c   270 g   199 t
ORIGIN
Query Match      77.3%; Score 545; DB 14; Length 1086;
Best Local Similarity 88.0%; Pred. No. 1.8e-130;
Matches 603; Conservative 0; Mismatches 81; Indels 1; Gaps 1;
QY 19 CTCCTGGGGCTCCTGCTGCTGCTGCCCTCCAGGTCACGATGCTCCCTATGAATGACTCAG 78
Db 19 |||||
QY 55 CTCCTCTCGGCTCTCTCTCACTGACAGGCTCTCTGACCTCTATGCTGACTCAG 114
Db 55 |||||
QY 79 CCACCTCGGTGTCACTGCTCCAGAGACAGCGCCAGGATCACCTGTGGGGAGACAAC 138
Db 79 |||||
QY 115 CCACCTCGGTGTCACTGCTCCAGAGACAGCGCCAGGATCACCTGTGGGGAGACAAC 173
Db 115 |||||
QY 139 ACTAGAAATCAATATCTCCACTGTTACGACGACGACGACGCGGCCCTTACTGCTC 198
Db 139 |||||
QY 174 ATTAGAGGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 233
Db 174 |||||
QY 199 ATCTATGATGATAGTACCGGCTCCTCAGGATCCCTGAGCGATTCTCTGGCTCCAAATCA 258
Db 199 |||||
QY 234 GTCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 293
Db 234 |||||
QY 259 GGGAAACACCGCCACCTGACATCAACCGGGTTCAGGCGGGGATGAGCTGACTATTAC 318
Db 259 |||||
QY 294 GAAACACCGCCACTCTGACCATCAGCAGGCTCGAGCGGGGATGAGGCGGACTATTAC 353
Db 294 |||||
QY 319 TGTGAGTGTGGACAGGCTAGTGATCATCCGGTCTTCGAGGAGGACCGGGTGACC 378
Db 319 |||||
QY 354 TGTGAGTGTGGACAGGCTAGTGATCATCCGGTCTTCGAGGAGGACCGGGTGACC 413
Db 354 |||||
QY 379 GTCTAGGTCAGCCCAAGGCTGCGGCTCGGTCACCTCTGTTCCCGCCCTCTCTGAGGAG 438
Db 379 |||||
QY 414 GTCTAGGTCAGCCCAAGGCTGCGGCTCGGTCACCTCTGTTCCCGCCCTCTCTGAGGAG 473
Db 414 |||||
QY 439 CTTCAAGCCAAACAGGCTCAGTGTGTCTCATTAAGTGAATTTCAACCGGGAGCGGTG 498
Db 439 |||||
QY 474 CTTCAAGCCAAACAGGCTCAGTGTGTCTCATTAAGTGAATTTCAACCGGGAGCGGTG 533
Db 474 |||||
QY 499 ACAGTGGCTTGAAGGAGATAGCAGCGGCTCAAGCGGGGATGAGGACCAACACCC 558
Db 499 |||||
QY 534 ACAGTGGCTTGAAGGAGATAGCAGCGGCTCAAGCGGGGATGAGGACCAACACCC 593
Db 534 |||||
QY 559 TCCAAACAAAGCAACAAAGTACGCGGCTCAGCAGCTACTGAGCCTGACGCTGAGCAG 618
Db 559 |||||
QY 594 TCCAAACAAAGCAACAAAGTACGCGGCTCAGCAGCTACTGAGCCTGAGCCTGAGCAG 653
Db 594 |||||
QY 619 TGAAGTCCACAGAGCTACAGTCCAGGTCACGATGAGGAGGACCGGTGGAGAAG 678
Db 619 |||||
QY 654 TGAAGTCCACAGAGCTACAGTCCAGGTCACGATGAGGAGGACCGGTGGAGAAG 713
Db 654 |||||
QY 679 ACAGTGGCTTGAAGGAGATAGCAGCGGCTCAAGCGGGGATGAGGACCAACACCC 703
Db 679 |||||
QY 714 ACAGTGGCTTGAAGGAGATAGCAGCGGCTCAAGCGGGGATGAGGACCAACACCC 738
Db 714 |||||

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```

RESULT 14
LOCUS      B0711587
DEFINITION B0711587 917 bp mRNA linear EST 16-JUL-2002
AGENCY     AGENCOURT_8475231 NIH_MGC 113 Homo sapiens cDNA clone IMAGE:6301461
5', mRNA sequence.
ACCESSION  B0711587
VERSION     B0711587.1 GI:21850486
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 917)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1998)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgabbs-remail.nih.gov  
 Tissue Procurement: Dr. Mark Watson  
 cDNA Library Preparation: Rubin Laboratory  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCW2517 row: f column: 22  
 High quality sequence stop: 552.

#### FEATURES

```

source
Location/Qualifiers
1..917
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH MGC 113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pORF7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 223 a 286 c 242 g 166 t
ORIGIN

```

```

Query Match      77.2%; Score 544.4; DB 14; Length 917;
Best Local Similarity 88.5%; Pred. No. 2.4e-130;
Matches 614; Conservative 0; Mismatches 76; Indels 4; Gaps 2;
QY 11 CGGCTCAGTCTCTGGGGCTCCTGCTGCTGCTGCCCTCCAGGTCACGATGCTGCTATGAAC 70
Db 11 |||||
QY 38 CGGTTCTCTCTCTGGGCTCTCTCTCACTG---CACAGGCGCTGTGACCTCTATGTGT 94
Db 38 |||||
QY 71 TGACTCAGCCACCTCTGGGTGTGAGTGTCCCAAGACAGACGCGCCAGGATCAGCTGTGGGG 130
Db 71 |||||
QY 95 TGACTCAGCCACCTCTGGGTGTGAGTGTCCCAAGACAGACGCGCCAGGATCAGCTGTGGGG 154
Db 95 |||||
QY 131 GAGACAAAGTAGAATGAATATGTCTGCTGCTGCTGCTGCCCTCCAGGTCACGATGCTGCTATGAAC 190
Db 131 |||||
QY 155 GGAACAAACATTGACAGTAAATGTAAATGTGTTACCGAGGCGCAGGCGGCCCCCTG 214
Db 155 |||||
QY 191 TACTGCTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 250
Db 191 |||||
QY 215 TGCTGCTGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 274
Db 215 |||||
QY 251 CCAATATCAGGGAACACCGCCACCTCTGACCATCAACGGGGTCCAGGCCCGGGATGAGGCTG 310
Db 251 |||||
QY 275 CCACCTCTGTTGATACGGCCACCTCTGACCATCAGTGTGTGTTGAAAGCGGGATGAGGCG 334
Db 275 |||||
QY 311 ACTATTACTGTGAGGTGTGGGACAGGCTAGTGATCATCCGGTCTTCGAGGAGGAGGCC 370
Db 311 |||||
QY 335 ACTACTACTGTGAGGTGTGGGATAGTACTGTGTTCAACGGGTCTTCGCGGAGGAGCA 394
Db 335 |||||
QY 371 GGGTGACCGTCTAGGTGAGCCCAAGGCTGCCCGCTCGGTCACTCTGTTCCCGCCCTCT 430
Db 371 |||||
QY 395 GGGTGACCGTCTCGGGGTGAGCCCAAGGCTGCCCGCTCGGTCACTCTGTTCCCGCCCTCT 454
Db 395 |||||
QY 431 CTGAGGAGCTTCAAGCCAAAGGCCACACTGGTGTGTCTATAAGTGAATTTCTACCCGG 490
Db 431 |||||
QY 455 CTGAGGAACTTCAAGCCAAAGGCCACACTGGTGTGTCTATAAGTGAATTTCTACCCGG 514
Db 455 |||||
QY 491 GAGCCGTGACAGTGTGCTGGAAGGAGGATAGCAGCCCGCTCAAGCGGGGAGTGGAGCA 550
Db 491 |||||
QY 515 GAGCCGTGACAGTGTGCTGGAAGGAGGATAGCAGCCCGCTCAAGCGGGGAGTGGAGCA 574
Db 515 |||||

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 13:14:13 ; Search time 157.546 Seconds  
(without alignments)  
10077.457 Million cell updates/sec

Title: US-09-576-424-1  
Perfect score: 705  
Sequence: 1 atgagggtcccgctagct.....ccctacagaatgttcata 705

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq\_101002.\*  
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2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	705	100.0	705	18 AAT62509	Primatized anti-hu
2	705	100.0	705	19 AAV35484	Macaque primatized
3	705	100.0	705	24 AAS17242	DNA sequence of a
4	585.2	83.0	702	18 AAT62867	Ant-CD4 monkey-hu
5	582.6	82.6	926	20 AAZ24427	Human bladder tumo
6	555.6	78.8	836	23 AAS83482	DNA encoding novel
7	540.2	76.6	711	19 AAV35488	Macaque primatized
8	540.2	76.6	711	24 AAS17246	DNA sequence of a
9	538.6	76.4	711	18 AAT62512	Primatized anti-hu

10	527.6	74.8	1027	24	ABQ54438	Human ovarian anti
11	524	74.3	841	23	AAS83486	DNA encoding novel
12	520.8	73.9	904	24	ABK28671	Human CDNA encodin
13	520.4	73.8	869	22	AAS22717	Human CDNA encodin
14	516	73.2	791	23	AAS87271	DNA encoding novel
15	515	73.0	1825	22	AAS22777	Human CDNA encodin
16	514.4	73.0	859	22	AAS22481	Human CDNA encodin
17	512.8	72.7	960	21	AAC78188	Human cancer assoc
18	512	72.6	872	9	AAN81655	VDJC regions of hu
19	511	72.5	654	22	AAS13364	Human CDNA encodin
20	509.2	72.2	930	22	AAS22541	Human CDNA encodin
21	506	71.8	793	23	AAS83481	DNA encoding novel
22	504	71.5	807	23	AAS83484	DNA encoding novel
23	495.2	70.2	863	24	ABK28650	Human CDNA encodin
24	480	68.1	849	22	AAH98186	Human EST-derived
25	474.2	67.3	884	11	AAQ03609	Sequence encoding
26	473.6	67.2	810	23	AAS87270	DNA encoding novel
27	473	67.1	935	22	AAC66525	Human immune syste
28	472	67.0	768	20	AAH06953	Monoclonal antibod
29	472	67.0	768	20	AAH06954	Monoclonal antibod
30	465.6	66.0	826	22	AAI58109	Human polynucleoti
31	462.8	65.6	915	24	ABN97248	Gene #3746 used to
32	462.8	65.6	915	24	ABK64815	Human benign prost
33	462.8	65.6	915	24	ABL65478	Lung cancer relate
34	462.2	65.6	654	14	AAQ49835	Anti-HIV-1 recombi
35	462	65.5	762	22	AAC84209	Plasmid Glambda-1B
36	462	65.5	5679	22	AAH84207	DNA encoding novel
37	461.8	65.5	889	23	AAS77073	Antibody D lambda
38	457	64.8	902	14	AAQ35100	Human immune syste
39	456	64.7	895	22	AAC66530	DNA encoding novel
40	455.6	64.6	763	23	AAS83480	Human immune syste
41	455.4	64.6	891	22	AAC66528	Human type antiHum
42	455.2	64.6	708	22	AAH47902	DNA encoding novel
43	453.6	64.3	783	23	AAS83483	DNA encoding novel
44	452	64.1	876	23	AAS83478	DNA encoding novel
45	451.6	64.1	651	19	AAV11293	Antibody HB4C5 lig

#### ALIGNMENTS

RESULT 1  
AAT62509  
ID AAT62509 standard; DNA; 705 BP.  
XX AC  
XX AAT62509;  
XX  
XX 25-MAY-1997 (first entry)  
XX  
XX Primatized anti-human B7.1 antigen antibody 7C10 light chain DNA.  
DE  
DE Monoclonal antibody; cynomolgus monkey; macaque; 7C10;  
KW Primatized antibody; B7 antigen; CD28; immunosuppressive;  
KW autoimmune disease; idiopathic thrombocytopenia purpura;  
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;  
KW type 1 diabetes mellitus; graft versus host disease;  
KW hetero-hybridoma; transfectoma; ss.  
XX  
XX Chimeric Macaca cynomolgus;  
OS Chimeric Homo sapiens.  
XX  
XX WO9640878-A1.  
XX  
XX 19-DEC-1996.  
XX  
XX 06-JUN-1996; 96WO-US10053.  
XX  
XX 07-JUN-1995; 95US-0487550.  
XX  
XX (IDEC-) IDEC PHARM CORP.  
XX  
XX Anderson DR, Brans P, Hanna N, Shestowsky WS;  
XX

DR WPI; 1997-108638/10.  
 XX P-PSDB; AAW01817.  
 PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -  
 XX useful for treating autoimmune disease or graft-versus-host disease  
 PS Claim 7; Fig 8A; 81pp; English.  
 XX  
 CC 2 DNA sequences (AAT62509 and AAT62510) respectively code for  
 CC primatised forms (AAW01817 and AAW01818) of the light and heavy chains  
 CC of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody  
 CC 7C10. Cloned 7C10 light and heavy variable genes are inserted into  
 CC an expression vector (pref. NEOSPLA) which contains human light and  
 CC heavy chain constant region genes to allow prodn. of primatised  
 CC antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1  
 CC antibodies have also been produced (see also AAW01819-22). The  
 CC primatised antibodies inhibit the B7:CD28 pathway, making them  
 CC useful immunosuppressants for the treatment of autoimmune disorders  
 CC and graft-versus-host disease.  
 XX  
 SQ Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;  
 Query Match 100.0%; Score 705; DB 18; Length 705;  
 Best Local Similarity 100.0%; Pred. No. 4e-167;  
 Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGGTCCCGCTCAGCTCCCTGGGGCTCCTGCTCTGGCTCCAGGTGCACGATGT 60  
 DB |||||  
 1 ATGAGGGTCCCGCTCAGCTCCCTGGGGCTCCTGCTCTGGCTCCAGGTGCACGATGT 60  
 QY 61 GCCTATGAATGACTAGTCCAGCCACCTCGGTGTAGTGTCCCGAGGACAGCGCCAGGATC 120  
 DB |||||  
 61 GCCTATGAATGACTAGTCCAGCCACCTCGGTGTAGTGTCCCGAGGACAGCGCCAGGATC 120  
 QY 121 ACCTGTGGGGGACACACAGTAGAATGATATGTCCACTGTACAGCAGAGCCAGCG 180  
 DB |||||  
 121 ACCTGTGGGGGACACACAGTAGAATGATATGTCCACTGTGTACAGCAGAGCCAGCG 180  
 QY 181 CGGGCCCTTATCTGCTCATCTATGATGATGACCGGCCCTCAGGGATCCCTGAGCGA 240  
 DB |||||  
 181 CGGGCCCTTATCTGCTCATCTATGATGATGACCGGCCCTCAGGGATCCCTGAGCGA 240  
 QY 241 TTCTCTGGTCCAAATCAGGGAACACCGGCACCTGACCATCAACGGGTGCGAGGCCGG 300  
 DB |||||  
 241 TTCTCTGGTCCAAATCAGGGAACACCGGCACCTGACCATCAACGGGTGCGAGGCCGG 300  
 QY 301 GATGAGGCTGACTATTACTGTGAGGTGTGGACAGGGCTAGTATCATCGGTCTTCGGA 360  
 DB |||||  
 301 GATGAGGCTGACTATTACTGTGAGGTGTGGACAGGGCTAGTATCATCGGTCTTCGGA 360  
 QY 361 GGAGGACCCGGGTGACCGCTCCTAGGTTCAGCCCAAGGCTGCCCTCGGTCACTCTGTTC 420  
 DB |||||  
 361 GGAGGACCCGGGTGACCGCTCCTAGGTTCAGCCCAAGGCTGCCCTCGGTCACTCTGTTC 420  
 QY 421 CGGCTCTCTCTGAGGAGCTTCAAGCCCAACAGGCCACACTGGTGTCTCTAAGTGAC 480  
 DB |||||  
 421 CGGCTCTCTCTGAGGAGCTTCAAGCCCAACAGGCCACACTGGTGTCTCTAAGTGAC 480  
 QY 481 TTCTACCCGGGACCGCTGACAGTGGCTTGAAGGCAGATAGACGCCCTGCAAGCGGGA 540  
 DB |||||  
 481 TTCTACCCGGGACCGCTGACAGTGGCTTGAAGGCAGATAGACGCCCTGCAAGCGGGA 540  
 QY 541 GTGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGGAGTACCTG 600  
 DB |||||  
 541 GTGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGGAGTACCTG 600  
 QY 601 AGCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACAGTCCAGGTTCACGATGAA 660  
 DB |||||  
 601 AGCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACAGTCCAGGTTCACGATGAA 660  
 QY 661 GGGAGCACCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 705  
 DB |||||  
 661 GGGAGCACCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 705

## RESULT 2

AAV35484

ID AAV35484 standard; DNA; 705 BP.

XX AC

XX AAV35484;

XX DT

XX 29-SEP-1998 (first entry)

XX DE

XX Macaque primatized 7C10 light chain DNA.

XX KW

Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;  
 CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;  
 T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;  
 immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;  
 T cell proliferation; ss.

XX OS

XX Macaca fascicularis.

XX FH

XX Key Location/Qualifiers

XX CDS

XX 1..705

XX /\*tag= a

XX /product= 7C10 light chain

XX FT

XX WO9819706-A1.

XX PD

XX 14-MAY-1998.

XX PF

XX 29-OCT-1997; 97WO-US19906.

XX PR

XX 08-NOV-1996; 96US-0746361.

XX XX

XX (IDEC-) IDEC PHARM CORP.

XX XX

XX Anderson DR, Brams P, Hanna N;

XX PI

XX WPI; 1998-286601/25.

XX DR

XX P-PSDB; AAW63760.

XX XX

New monoclonal antibodies specific for B7.1 or B7.2 antigens and  
 inhibiting binding to CD28 - useful as specific immunosuppressants  
 for treating diseases that involve interactions between T and B  
 cells, e.g. graft rejection or tumours

XX PT

XX Example 7; Fig 3a; 87pp; English.

XX PS

This sequence encodes a primatized form of the antibody 7C10 light chain  
 from macaque. This sequence is used in a method which studies new  
 monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to  
 B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such  
 Mab's are specific immunosuppressants for treatment of diseases involving  
 T cell/B cell interactions, particularly autoimmune disease, specifically  
 idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type  
 I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,  
 inflammatory bowel disease, allergy and multiple sclerosis, graft vs.  
 host diseases, B cell lymphoma, infections (including by human immune  
 deficiency virus) or inflammatory disease and tumours. Optionally the  
 Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can  
 also be used as imaging agents and as vaccines or immunogens to develop  
 anti-idiotypic reagents. Mab's are optionally combined with other proteins  
 or small molecule immunosuppressants. Blocking B7/CD28 interactions  
 induces long-term, antigen-specific immunosuppression, i.e. it inhibits  
 production of interleukin-2 (IL-2), T cell proliferation and  
 antigen-specific immunoglobulin G (IgG) responses.

XX SQ

Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

XX Query Match

Best Local Similarity 100.0%; Score 705; DB 19; Length 705;

XX Matches

705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1

ATGAGGGTCCCGCTCAGCTCCCTGGGGCTCCTGCTCTGGCTCCAGGTGCACGATGT 60

Db	1	ATGAGGGTCCCGGCTCAGCTCCTGGGGTCTCTGGCTCTGGCTCCGAGGTGACGATGT	60
Qy	61	GCCTATGAACGTACTCAGCCACCCCTCGTGTCCAGTGTCCCAAGGACAGACGCGCAGGATC	120
Db	61	GCCTATGAACGTACTCAGCCACCCCTCGTGTCCAGTGTCCCAAGGACAGACGCGCAGGATC	120
Qy	121	ACCTGTGGGGAGACAAACAGTAGAAATGAATGTCCATGTGTACACAGAGAAGCCAGCG	180
Db	121	ACCTGTGGGGAGACAAACAGTAGAAATGAATGTGTCCATGTGTACACAGAGAAGCCAGCG	180
Qy	181	CGGGCCCTATACTGGTCATCTATGATGATGATGACCGGCCCTCAGGGATCCCTGAGCGA	240
Db	181	CGGGCCCTATACTGGTCATCTATGATGATGATGATGACCGGCCCTCAGGGATCCCTGAGCGA	240
Qy	241	TTCTCTGGCTCCAAATCAGGGAACACCGCCACCTTGACCATCAAAGGGGTTCAGAGCCGGG	300
Db	241	TTCTCTGGCTCCAAATCAGGGAACACCGCCACCTTGACCATCAAAGGGGTTCAGAGCCGGG	300
Qy	301	GATGAGGTGACTATTACTGTCAAGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGA	360
Db	301	GATGAGGTGACTATTACTGTCAAGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGA	360
Qy	361	GGAGGACCCGGGTGACCGTCTTAGGTGAGCCCAAGGCTGCCCTCGGTCACTCTGTTC	420
Db	361	GGAGGACCCGGGTGACCGTCTTAGGTGAGCCCAAGGCTGCCCTCGGTCACTCTGTTC	420
Qy	421	CCGGCCCTCTCTGAGGAGCTTCAAGCCAAACAGGCGCACACTGGTGTCTCATAAAGTGAC	480
Db	421	CCGGCCCTCTCTGAGGAGCTTCAAGCCAAACAGGCGCACACTGGTGTCTCATAAAGTGAC	480
Qy	481	TTCTACCCGGGAGCCGTGACAGTGGCCCTGGAAAGGCAGATAGCAGCCCCCTCAAGCGCGA	540
Db	481	TTCTACCCGGGAGCCGTGACAGTGGCCCTGGAAAGGCAGATAGCAGCCCCCTCAAGCGCGA	540
Qy	541	GTGGAGACCAACACACCTCCAAAACAAAGCAACACAGTACGGGCCACAGCTACCTTG	600
Db	541	GTGGAGACCAACACACCTCCAAAACAAAGCAACACAGTACGGGCCACAGCTACCTTG	600
Qy	601	AGCCTGACCGCTGAGCAGTGGAAAGTCCCAACAGAAGCTACAGCTGCCAGGTACAGATGAA	660
Db	601	AGCCTGACCGCTGAGCAGTGGAAAGTCCCAACAGAAGCTACAGCTGCCAGGTACAGATGAA	660
Qy	661	GGGAGCACCGTGGAGAGACAGTGGCCCCCTACAGAAATGTTATGA	705
Db	661	GGGAGCACCGTGGAGAGACAGTGGCCCCCTACAGAAATGTTATGA	705

RESULT 3

RESULT 3  
AAS17242

AAS17242  
ID AAS17242 standard; DNA; 705 BP.

XX  
XX

AC AAS17242;

XX

DT 12-MAR-2002 (first entry)

XX DE DNA sequence of a primatised form of the light chain of 7C10 antibody.

Human; macaque monkey; light chain; primatised antibody; 7C10 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs.-host disease; immunosuppression; organ rejection; interleukin-2; IL-2; mutant; ds.

**XX**

OS Chimeric - Homo sapie

OS Chimeric -

OS Synthetic.

XX	Key	Location/Outfit
EH		

FH	Key	Location/Qualifiers
FT	CDS	1 705

```

CDS
1..705
/*tag= a

```

```

FT      /tag= a
FT      /product= "Light chain of 7C10 antibody"

```

1. FOR THE PURPOSES OF THIS ORDER, THE FOLLOWING DEFINITIONS SHALL APPLY:

[illegible]

WO200109567-A1.  
29-NOV-2001.  
22-MAY-2001; 2001WO-US16364.  
22-MAY-2000; 2000US-0576424.  
(IDEC-) IDEC PHARM CORP.  
Anderson DR, Hanna N, Brams P;  
WPI; 2002-089895/12.  
P-PSDB; AAU11538.

Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as allergy -

Example 8; Fig 3a; 89pp; English.

The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, and autoimmune diseases such as idiopathic thrombocytopenia purpura, systemic lupus, erythematosis, type 1 diabetes mellitus, rheumatoid arthritis, psoriasis; aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food-related allergies e.g. migraine, rhinitis and eczema, and other types of allergies. The present nucleic acid sequence encodes the light chain of 7C10, a primatised antibody used in the invention to induce apoptosis and inhibit production of interleukin-2 (IL-2).

Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

Very Match 100.0%; Score 705; DB 24; Length 705;  
1st Local Similarity 100.0%; Pred. No. 4e-167;  
tches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 ATGAGGGTCCCGCTCAGCTCCTCGGGCTCTGTGCTCTCGCTCCAGGTGCAGATGT 60  
1 ATGAGGGTCCCGCTCAGCTCCTCGGGCTCTGTGCTCTCGCTCCAGGTGCAGATGT 60  
61 GCCTATGAACCTGACTCAGCCACCCTCGGTGTGTCAGTGTCCCGAGGACAGCGCCAGGATC 120  
61 GCCTATGAACCTGACTCAGCCACCCTCGGTGTGTCAGTGTCCCGAGGACAGCGCCAGGATC 120  
121 ACCTGTGGGGGAGACAAACAGTAGAAATGAATATGTTCATCGGTACAGAGACGACG 180  
121 ACCTGTGGGGGAGACAAACAGTAGAAATGAATATGTTCATCGGTACAGAGACGACG 180  
181 CGGGCCCTTACTACTGGTTCATCTATGATCATAGTAGACCGGCCCTCAGGGATCCCTCAGGCG 240  
181 CGGGCCCTTACTACTGGTTCATCTATGATCATAGTAGACCGGCCCTCAGGGATCCCTCAGGCG 240  
241 TTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTTCAGGCCCGG 300  
241 TTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTTCAGGCCCGG 300  
301 GATGAGGCTGACTATTACTGTGTCAGGTGTGGACAGGGGCTAGTGATCATCCGGTCTTCGGA 360  
301 GATGAGGCTGACTATTACTGTGTCAGGTGTGGACAGGGGCTAGTGATCATCCGGTCTTCGGA 360

QY 361 GGAGGACCGGGTGAACCGTCTAGGTCAAGCCCAAGGCTGCCCCCTGGTCACTCTGTTTC 420  
 Db 361 GGAGGACCGGGTGAACCGTCTAGGTCAAGCCCAAGGCTGCCCCCTGGTCACTCTGTTTC 420  
 QY 421 CGGCGCTCTCTCAGGAGCTTCAAGCCCAAGGCTGCCCCCTGGTCACTCTGTTTC 480  
 Db 421 CGGCGCTCTCTCAGGAGCTTCAAGCCCAAGGCTGCCCCCTGGTCACTCTGTTTC 480  
 QY 481 TTCTACCGGGAGCGGTGACAGTGGCTGGAAGGCGAGATAGCAGCCCGTCAAGGCGGGA 540  
 Db 481 TTCTACCGGGAGCGGTGACAGTGGCTGGAAGGCGAGATAGCAGCCCGTCAAGGCGGGA 540  
 QY 541 GTGAGACCAACACACCCCTCCAAACAAAGCAACAAAGTACCGCGCCAGCAGCTACCTG 600  
 Db 541 GTGAGACCAACACACCCCTCCAAACAAAGCAACAAAGTACCGCGCCAGCAGCTACCTG 600  
 QY 601 AGCCTGACGCTGAGCAGTGGAGTCCACAGAGCTACAGCTGCGCAGGTCAAGCATGAA 660  
 Db 601 AGCCTGACGCTGAGCAGTGGAGTCCACAGAGCTACAGCTGCGCAGGTCAAGCATGAA 660  
 QY 661 GGGAGCACCGTGGAGAGACAGTGGCGCCCTACAGAGTGTTCATGA 705  
 Db 661 GGGAGCACCGTGGAGAGACAGTGGCGCCCTACAGAGTGTTCATGA 705

# RESULT 4 AAT62867

ID AAT62867 standard; DNA; 702 BP.

AC AAT62867;

XX 18-OCT-1997 (first entry)

XX Ant-CD4 monkey-human chimeric antibody CE9.1 DNA.

XX CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;  
 KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;  
 KW leukaemia; lymphoma; graft-versus-host disease; asthma;  
 XX transplant rejection; HIV; therapy; CE9.1; ss.

OS Chimaeric Macaca cynomolgus;  
 OS Chimaeric Homo sapiens.

XX WO9709351-A1.

XX 13-MAR-1997.

XX 05-SEP-1996; 96WO-US14324.

XX 06-SEP-1995; 95US-0523894.

XX (IDEC-) IDEC PHARM CORP.

XX Hanna N, Newman RA, Reff ME;

XX WPI; 1997-201913/18.

XX P-PSDB; AAW14924.

PT Chimeric antibody comprising monkey variable domains and human  
 PT constant domains - affects CD4-mediated immune functions, esp.  
 PT useful for treatment of autoimmune disease, e.g. rheumatoid  
 PT arthritis

XX Example 1; Page 79-80; 155pp; English.

XX A DNA sequence (AAT62867) codes for lambda variable and constant  
 CC domains (AAW14924) of anti-human CD4 monkey/human chimeric antibody  
 CC CE9.1. This antibody contains the antigen binding domains (see  
 CC also AAW14922-23) of a cynomolgus monkey anti-CD4 monoclonal  
 CC antibody, a human heavy chain constant region of gamma 1 isotype  
 CC and Gm1a, Gm1z allotype, and a human lambda light constant region  
 CC of the O2 minus, mcg minus genotype and ke minus allotype. The  
 CC immunoglobulin genes were cloned into mammalian expression vector

CC TCAC 6, and chimeric antibody was produced in CHO cells. CE9.1  
 CC binds to domain 1 of human, but not macaque, CD4, a region involved  
 CC in the interaction with MHC Class II molecules on antigen-  
 CC presenting cells. It shows potent immunomodulatory activity with  
 CC low immunogenicity in humans, and can be used to treat autoimmune  
 CC diseases such as rheumatoid arthritis.

XX SQ Sequence 702 BP; 151 A; 217 C; 207 G; 127 T; 0 other;

Query Match 83.0%; Score 585.2; DB 18; Length 702;

Best Local Similarity 89.6%; Pred. No. 4.2e-137; Indels 0; Gaps 0;

Matches 629; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 4 AGGGTCCCGGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCGAGTGCAGATGTC 63

Db 1 ATGGCTGGGCTCTGCTGCTCCTGGGCTCCTGCTCACTTACAGACTCTGGGCTCC 60

QY 64 TATGAATGACTCAGCAGCCCTCGGTGTGTCAGTGTCCAGGACAGAGCCAGGATCACC 123

Db 61 TATGATTTAGTTCAGCTCGCTCAGTGTCCGTTGCTCCAGGACAGAGCCGCGGTTTACC 120

QY 124 TGTGGGGAGACAAACAGTAGAATGAATATGTCCACTGTGTACAGAGGACAGCGCG 183

Db 121 TGTGGGGAGACAAACAGTTGGAAGGAAAGTGTACAGTGTGTACAGAGGACAGCGCAG 180

QY 184 GCCCTTATATCTGCTCATCTATGATGATGTGACCGGCTCAGGGATCCTCAGCGATTTC 243

Db 181 GCCCTTGTGCTGCTCATCTATGCTGACAGGAAAGGCTCAGGGATCCTCAGCGATTTC 240

QY 244 TCTGGTCCAAATCAGGGAAACACCGCCACCTGTGACATCAACAGGGGTGAGGCGGGGAT 303

Db 241 TCTGGTCCAACTCAGGGAAACACCGCCACCTGTGACATCAGCGGGGTGAGGCGGGGAT 300

QY 304 GAGGCTGACTATTACTGTGAGGTGGGACAGGGGTAGTGATCATCCGCTCTTCGGAGGA 363

Db 301 GAGGCTGACTATTACTGTGAGGTGGGACAGGTACTGTGATCATTCGGGCGGA 360

QY 364 GGGACCCGGGTGACCGTCTTAGGTGAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCG 423

Db 361 GGGACCCGGGTGACCGTCTTAGGTGAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCG 420

QY 424 CCTCTCTGTGAGGAGTTCAAGCCCAAGGCGCACACTGTTGTGTCTCATAGTGAATTTC 483

Db 421 CCTCTCTGTGAGGAGTTCAAGCCCAAGGCGCACACTGTTGTGTCTCATAGTGAATTTC 480

QY 484 TACCCGGGAGCGGTGACAGTGGCTGGAGGAGGAGATAGCAGCCCGTCAAGCGGAGTG 543

Db 481 TACCCGGGAGCGGTGACAGTGGCTGGAGGAGGAGATAGCAGCCCGTCAAGCGGAGTG 540

QY 544 GAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCTACCTGAGC 603

Db 541 GAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCTACCTGAGC 600

QY 604 CTGACGCTGAGCAGTGGAGTCCACAGAGCTCAGCTGCGCAGGTCAAGCATGAAGG 663

Db 601 CTGACGCTGAGCAGTGGAGTCCACAGAGCTCAGCTGCGCAGGTCAAGCATGAAGG 660

QY 664 AGCACCGTGGAGAGACAGTGGCGCCCTACAGAGTGTTCATGA 705

Db 661 AGCACCGTGGAGAGACAGTGGCGCCCTACAGAGTGTTCATGA 702

## RESULT 5

AAZ24427

ID AAZ24427 standard; cDNA; 926 BP.

XX AAZ24427;

XX 14-FEB-2000 (first entry)

XX Human bladder tumour cDNA library derived EST 39.

XX Expressed sequence tag; human; bladder; tumour; cancer; cytostatic;



KW treatment; gene therapy; EST; ss.  
 XX Homo sapiens.  
 XX DE19818619-A1.  
 XX PN  
 XX PD  
 XX 28-OCT-1999.  
 XX  
 PF 21-APR-1998; 98DE-1018619.  
 XX  
 PR 21-APR-1998; 98DE-1018619.  
 XX  
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
 XX  
 PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;  
 XX  
 DR WPI; 1999-612028/53.  
 XX  
 XX New nucleic acid sequences expressed in bladder tumor tissue, and  
 PT derived polypeptides, for treatment of bladder tumor and identification  
 PT of therapeutic agents -  
 XX  
 PS Claim 3; Page 90; 132pp; German.  
 XX  
 CC This invention describes novel polypeptide fragments (I) and the  
 CC polynucleotides (II) that encode them that are highly expressed in a  
 CC human bladder tumour and which have cytostatic activity. (III) are used  
 CC for recombinant expression of (I) and to isolate complete genes. (I) are  
 CC used to identify agents suitable for treatment of bladder cancer, to  
 CC directly treat this form of cancer (including expression from gene  
 CC therapy vectors) or are used in a preparation for cancer treatment. (I)  
 CC is also used for the generation of specific antibodies. (II) are  
 CC identified by assembling ESTs (expressed sequence tags) from a  
 CC particular tissue type before comparison of expression patterns. This  
 CC allows a significantly longer fragment of the gene to be revealed, and  
 CC therefore reduces the number of failures associated with the fact that  
 CC ESTs from different libraries may represent different parts of the same  
 CC unknown gene, distorting the estimated frequency of occurrence in a  
 CC particular tissue. AA243260-243309 represent expressed sequence tag (EST)  
 CC fragments isolated from a human bladder tumour cDNA library which encode  
 CC the proteins represented in AA243260-243309.  
 XX  
 SQ Sequence 926 BP; 249 A; 275 C; 240 G; 162 T; 0 other;  
 Query Match 82.6%; Score 582.6; DB 20; Length 926;  
 Best Local Similarity 94.1%; Pred. No. 2e-136;  
 Matches 604; Conservative 0; Mismatches 38; Indels 0; Gaps 0;  
 QY 62 CCTATGAACCTGACTAGCCACCCCTCGGTGTCAGTGTCCCGCAGACAGAGCCGAGATCA 121  
 DB 95 CCTATGTGCTGACTAGCCACCCCTCGGTGTCAGTGTCCCGCAGACAGAGCCGAGATTA 154  
 QY 122 CTTGTGGGGGAGACACAGTAGAATAATATCTCCACTGGTACACAGCAGAGCCAGCGC 181  
 DB 155 CTTGTGGGGGAAACAATTTGGAAGTAAAGTGTGCATCTGGTACACAGCAGAGCCAGGCC 214  
 QY 182 GGGCCCCCTTACTGTGTCATCTATGATGATAGTACCGGCCCTCAGGATCCCTGAGCGAT 241  
 DB 215 AGGCCCCCTGTGCTGCTGTATGATGATAGCAGCCGCCCTCAGGATCCCTGAGCGAT 274  
 QY 242 TCTTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACAGGGGTGAGCGCGGG 301  
 DB 275 TCTTGGCTCCAACTCTGGGAACACCGCCACCTGACCATCAACAGGGGTGAGCGCGGG 334  
 QY 302 ATGAGGCTCACTATTACTCTCAGGTGTGGACAGGGCTAGTATCATCGGCTTCGGAG 361  
 DB 335 ATGAGGCGCACTATTACTCTCAGGTGTGGATAGTATGATGATCATCGGCTTCGGCG 394  
 QY 362 GAGGAGCCCGGGTGACCGTCTAGGTGAGCCCAAGGCTGCCCTCGGTCACTCTCTTC 421  
 DB 395 GAGGAGCAACAGTACCGCTCTAGGTGAGCCCAAGGCTGCCCTCGGTCACTCTCTTC 454  
 QY 422 CGCCCTCTCTGAGGAGCTTCAAGCCCAAGCCACACTGGTGTCTCTATAAGTGACT 481

Db 455 CGCCCTCTCTGAGGAGCTTCAAGCCCAAGCCCACTGGTGTCTCTATAAGTGACT 514  
 QY 482 TCTACCCCGGAGCGGTGACAGTGGCTGGAAGCAGATAGCAGCCCGCTCAAGCGCGGAG 541  
 Db 515 TCTACCCCGGAGCGGTGACAGTGGCTGGAAGCAGATAGCAGCCCGCTCAAGCGCGGAG 574  
 QY 542 TGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACCGGGCCAGCAGACTACTGA 601  
 Db 575 TGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACCGGGCCAGCAGACTACTGA 634  
 QY 602 GCTGACCGCTGAGCAGTGGAGTCCACAGAGCTACAGCTGCCAGGTACCCATGAAG 661  
 Db 635 GCTGACCGCTGAGCAGTGGAGTCCACAGAGCTACAGCTGCCAGGTACCCATGAAG 694  
 QY 662 GGAGCACCGCTGAGAGAGACAGTGGCCCTTACAGAATGTTTCAT 703  
 Db 695 GGAGCACCGCTGAGAGAGACAGTGGCCCTTACAGAATGTTTCAT 736

RESULT 6  
 AAS83482  
 ID AAS83482 standard; cDNA; 836 BP.  
 XX  
 AC AAS83482;  
 XX  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE DNA encoding novel human diagnostic protein #19286.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US08631.  
 XX  
 PR 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI; 2001-639362/73.  
 DR P-PSDB; ABG19295.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -  
 XX  
 PS Claim 1; SEQ ID No 19286; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity







PA (HUMA-) HUMAN GENOME SCI INC.  
 XX Birse CE, Rosen CA;  
 XX WPI; 2002-147878/19.  
 DR P-PSDB; ABP41361.  
 DR XX  
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.  
 PT ovarian cancer), immune disorders, cardiovascular disorders and  
 PT neurological diseases -  
 XX  
 XX Claim 1; SEQ ID No 318; 2922pp; English.  
 XX  
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
 CC to the sequences of the invention. The invention additionally relates to  
 CC recombinant vectors and host cells comprising human ovarian antigen  
 CC polynucleotides, antibodies against human ovarian antigens, and the use  
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
 CC treating, prognosing or preventing various ovary and/or breast-related  
 CC disorders. Such conditions include ovarian cancer and breast cancer, and  
 CC metastatic tumours of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g., congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents cDNA encoding a human ovarian antigen of the  
 CC invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 1027 BP; 253 A; 306 C; 264 G; 192 T; 12 other;  
 SQ  
 Query Match: 74.8%; Score 527.6; DB 24; Length 1027;  
 Best Local Similarity 89.7%; Pred. No. 1.2e-122;  
 Matches 576; Conservative 3; Mismatches 57; Indels 6; Gaps 1;  
 QY 62 CCTATGAACCTGACTCAGCCACCTCGGTGTCACTGTCCCGCAGACAGCGCCGAGATCA 121  
 DB 192 CCTATGAGTGTACTCAGCCACCTCGGTGTCCCGCAGACAGCGCCGAGATCA 251  
 QY 122 CTGTGGGGAGACACAGTAGAATATGATATGTCCTGGTACCGAGAGAGCCAGCCG 181  
 DB 252 CTGTCTCGAGATAAATGGGGGATAATATCTTGTGTATCAGCAGAGCCAGGCC 311  
 QY 182 GGGCCCTATACGTGTCATGTATGATAGTACCGGCCCTCAGGATCCCTGACGAT 241  
 DB 312 AGTCCCTGTGTGGTCACTATCAAGATAACACCGGCCCTCAGGATCCCTGACGAT 371  
 QY 242 TCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCCGAGCCGGG 301  
 DB 372 TCTCTGGCTCCAACTTGGGACACAGCCACTCTGACATCAGCGGACCCAGGTATGG 431  
 QY 302 ATGAGGTGACTATTAATGTGAGGTGTGGGACAGGCTAGTATATCCGGTCTTCGGAG 361  
 DB 432 ATGAGGTGACTATTAATGTGAGGTGTGGGACAGGCTAGTATATCCGGTCTTCGGAG 485  
 QY 362 GAGGAGCCGGGTGACCGTCTAGGTGAGCCCAAGCTGCCCCCTCGGTCACTCTGTTCC 421  
 DB 486 GAGGAGCCAGCTGACCGTCTAGGTGAGCCCAAGCTGCCCCCTCGGTCACTCTGTTCC 545  
 QY 422 CGCCCTCTCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGTGTGTCTCTATAAGTACT 481  
 DB 546 CGCCCTCTCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGTGTGTCTCTATAAGTACT 605  
 QY 482 TCTACCCGGGAGCCGTGACAGTGGCTGGAAGGAGATAGCAGCCCCCTCAAGGGCGGAG 541  
 DB 606 TCTACCCGGGAGCCGTGACAGTGGCTGGAAGGAGATAGCAGCCCCCTCAAGGGCGGAG 665  
 QY 542 TGGAGACACACACACCTCCAAACAAAGCAACAAAGTACCGCGGCAGCAGCTACTCTGA 601  
 DB 666 TGGAGACACACACACCTCCAAACAAAGCAACAAAGTACCGCGGCAGCAGCTACTCTGA 725  
 QY 602 GCCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTTACAGTGCAGGCTGACGCATGAAG 661  
 DB 726 GCCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTTACAGTGCAGGCTGACGCATGAAG 785  
 QY 662 GGAGCACCGTGGAGAGACAGTGGGCCCTTACAGATGTTTCAT 703  
 DB 786 GGAGCACCGTGGAGAGACAGTGGGCCCTTACAGATGTTTCAT 827  
 RESULT 11  
 AAS83486  
 ID AAS83486 standard; cDNA; 841 BP.  
 XX  
 AC AAS83486;  
 XX  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE DNA encoding novel human diagnostic protein #19290.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US08631.  
 XX  
 PR 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI; 2001-639362/73.  
 P-PSDB; ABG19299.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -  
 XX  
 PS Claim 1; SEQ ID No 19290; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human  
 CC diagnostic coding sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 841 BP; 191 A; 273 C; 224 G; 153 T; 0 other;

Query Match 74.3%; Score 524; DB 23; Length 841;  
 Best Local Similarity 89.7%; Pred. No. 9.3e-122;  
 Matches 576; Conservative 0; Mismatches 60; Indels 6; Gaps 1;

QY 62 CCTATGACTGACTCAGCCACCTCGGTGTCAGTGTCCCGCAGACAGCGCCAGGATCA 121  
 DB 82 CCTATGACTGACTCAGCCACCTCGGTGTCAGTGTCCCGCAGACAGCGCCAGGATCA 141  
 QY 122 CCGTGGGGAGACACAGTAGAATCAATATCTCCACTGGTACCAAGCAGACAGCGCG 181  
 DB 142 CCGTGGGGAGACACAGTAGAATCAATATCTCCACTGGTACCAAGCAGACAGCGCG 201  
 QY 182 GGGCCCCCTATCTGTCATCTATGATGATAGTACCGCGCCCTCAGGGATCCCTGAGCGAT 241  
 DB 202 ACTCCCTGTCGTGTCATCTTTCAAGATAGCAAGCGCCCTCAGGGATCCCTGAGCGAT 261  
 QY 242 TCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTGGAGCGGGG 301  
 DB 262 TCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTGGAGCGGGG 321  
 QY 302 ATGAGGTGACTATTACTGTCAGTGTGGACAGGGCTAGTGATCATCCGGTCTTCGGAG 361  
 DB 322 ATGAGGTGACTATTACTGTCAGTGTGGACAGGGCTAGTGATCATCCGGTCTTCGGAG 375  
 QY 362 GAGGGACCCGGGTGACCGTCTTAGTGTGAGCCAGCGCCCTCGGTGTCATCTCTTTC 421  
 DB 376 GAGGGACCCGGGTGACCGTCTTAGTGTGAGCCAGCGCCCTCGGTGTCATCTCTTTC 435  
 QY 422 CGCCCTCTCTGAGGAGTTCAGCCCAACAGGCCACACTGGTGTGTCTATAGTGACT 481  
 DB 436 CGCCCTCTCTGAGGAGTTCAGCCCAACAGGCCACACTGGTGTGTCTATAGTGACT 495  
 QY 482 TCTACCGGAGCGGTGACAGTGGCTTGAAGCAGATAGCAGCCCGTCAAGCGGGAG 541  
 DB 496 TCTACCGGAGCGGTGACAGTGGCTTGAAGCAGATAGCAGCCCGTCAAGCGGGAG 555  
 QY 542 TGGAGACCCACACACCTCCAAACAAAGCAACAGTACGCGGGCCAGCAGCTACCTGA 601  
 DB 556 TGGAGACCCACACACCTCCAAACAAAGCAACAGTACGCGGGCCAGCAGCTACCTGA 615  
 QY 602 GCTTGAGCCTGAGCAGTGAAGTCCACAGAGCTTACAGTCCAGGTACCGCATGAAG 661  
 DB 616 GCCTGAGCCTGAGCAGTGAAGTCCACAGAGCTTACAGTCCAGGTACCGCATGAAG 675  
 QY 662 GGAGCACCGTGGAGAGACAGTGGCCCTACAGATGTTTCAT 703  
 DB 676 GGAGCACCGTGGAGAGACAGTGGCCCTACAGATGTTTCAT 717

## RESULT 12

ABK28671

ID ABK28671 standard; cDNA; 904 BP.

XX AC ABK28671;

XX XX

DT 09-APR-2002 (first entry)

XX XX

DE Human cDNA encoding secreted protein SECP38.

XX Human; ss; gene; SECP; antiinflammatory; cytostatic; cardiant;

KW immunosuppressive; antiviral; anti-HIV; antiarthritic; antirheumatic;

KW muscular active general; anticonvulsant; nootropic; neuroprotective;  
 KW antiallergic; hypotensive; cardiovascular disorder; atherosclerosis;  
 KW hypertension; myocardial infarction; autoimmune disorder;  
 KW inflammatory disorder; AIDS; acquired immunodeficiency syndrome;  
 KW allergy; rheumatoid arthritis; cell proliferative disorder; cancer;  
 KW developmental disorder; Duchenne muscular dystrophy;  
 KW neurological disorder; epilepsy; Alzheimer's disease.

XX Homo sapiens.

XX OS

PN WO200198353-A2.

XX XX

PD 27-DEC-2001.

XX XX

PF 20-JUN-2001; 2001WO-US19862.

XX XX

PR 20-JUN-2000; 2000US-212890P.

PR 23-JUN-2000; 2000US-213466P.

PR 27-JUN-2000; 2000US-214601P.

PR 31-JUL-2000; 2000US-222372P.

PR 08-SEP-2000; 2000US-231435P.

PR 15-SEP-2000; 2000US-232889P.

XX XX

PA (INCY-) INCYTE GENOMICS INC.

XX XX

PI Hillman JL, Tang YT, Yue H, Elliott VS, Tribouley CM, Lee EA;

PI Ramkumar J, Lal P, Xu Y, Warren BA, Hafalia AJA, Baughn MR;

PI Azinzei Y, Batra S, Burford N, Yao MG, Nguyen DB, Lu DM;

PI Wallia NK, Gandhi AR, Au-Young J, Patterson C;

XX XX

DR WPI; 2002-090431/12.

DR P-PSDB; AAU82012.

XX XX

PT Forty four human secreted proteins (referred to as SECP-1 to SECP-44),

PT useful in the diagnosis, treatment and prevention of cardiovascular

PT (e.g. atherosclerosis), autoimmune/inflammatory (e.g. allergies) and

PT cell proliferative disorders -

XX XX

PS Claim 5; Page 190; 195pp; English.

XX XX

CC The invention relates to forty four human secreted proteins (referred to

CC as SECP-1 to SECP-44) and the nucleic acids encoding them. Also

CC included are a host cell transformed with the nucleic acid, a

CC transgenic animal comprising the nucleic acid, an anti-SECP

CC antibody, use of the SECP proteins in isolating agonists and antagonists

CC of SECP activity and a method of isolating compounds which alter the

CC expression of the SECP nucleic acid. The SECP polynucleotides and

CC polypeptides are useful in the diagnosis, treatment and prevention of

CC cardiovascular (e.g. atherosclerosis, hypertension, myocardial

CC infarction), autoimmune/inflammatory (e.g. acquired immunodeficiency

CC syndrome (AIDS), allergies, rheumatoid arthritis), cell proliferative

CC (e.g. cancer), developmental (e.g. Duchenne and Becker muscular

CC dystrophy), and neurological (e.g. epilepsy, Alzheimer's disease)

CC disorders. Numerous other examples of each disorder are given in the

CC specification. The present sequence is a cDNA encoding a SECP protein.

XX XX

SQ Sequence 904 BP; 225 A; 281 C; 231 G; 167 T; 0 other;

Query Match 73.9%; Score 520.8; DB 24; Length 904;  
 Best Local Similarity 84.0%; Pred. No. 6e-121;  
 Matches 588; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 4 AGGGTCCCGCTCAGCTCCTGGGGCTCTGCTGCTGCTGCTGCCAGGTGCACGATGTGC 63  
 DB 54 ATGGCTTGACCCCTCTCTGCTGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 113  
 QY 64 TATGAATGACTCAGCCACCTCTCGGTGTGTCAGTGTCCCCAGGACAGACGGCCAGGATCACC 123  
 DB 114 TATGAGTGACACAGCCACCTCTCGGTGTGTCAGTGTCCCCAGGACAGACGGCCAGGATCACC 173  
 QY 124 TGTGGGGAGACAAACAGTAGAATGATATGTCCTGTCAGTGTCCCCAGGACAGACGGCCAGG 183  
 DB 174 TGCTCTGGAGATGTCATTGCCAAAAAATATGTTTATGTTACAGACAGAGTCAGGCCAG 233





QY 602 GCTGACGCTGAGCTGGAAGTCCACAGAGCTACAGTCCAGGTCACCCATGAAG 661  
Db 252 GCTGACGCTGAGCTGGAAGTCCACAGAGCTACAGTCCAGGTCACCCATGAAG 193  
QY 662 GGAACACCGTGGAGACAGCTGGCCCTACAGATGTTTCAT 703  
Db 192 GGAGCACCGTGGAGAGACAGTGGCCCTACAGATGTTTCAT 151

RESULT 14

AAS87271  
ID AAS87271 standard; cDNA; 791 BP.  
XX  
AC AAS87271;  
DT 13-FEB-2002 (first entry)  
XX  
DE DNA encoding novel human diagnostic protein #23075.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.  
DR P-PSDB; ABG23084.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX  
PS Claim 1; SEQ ID No 23075; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64157-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 791 BP; 183 A; 252 C; 208 G; 148 T; 0 other;

Query Match 73.2%; Score 516; DB 23; Length 791;  
Best Local Similarity 88.9%; Pred. No. 9.3e-120;

Matches 571; Conservative 0; Mismatches 65; Indels 6; Gaps 1;  
QY 62 CCTATGAATGACTCAGCCACCCCTCGGTGTAGTGTCCCCAGGACAGCGCCAGATCA 121  
Db 68 CCTATGAGTTGACTCAGCCACCCCTCAGTGTCCCGTGTCCCCAGGACAGCGCCAGATCA 127  
QY 122 CTTGTGGGGGAGACAAACAGTGAATATGTCTCAGTGTACAGGACAGGACCCAGCGC 181  
Db 128 CTTGTCTTGGAGATAAATTTGGGTGATAATATTTCTTGTGGTGTATCAGCAGAAAGCCGGCC 187  
QY 182 GGGCCCTTACTGTCTATGATAGTACCGGCCCTCAGGGATCCCTGAGCGAT 241  
Db 188 AGTCCCTCTACTGTCTGTATCAGATACCAACCGGCCCTCAGGGATCCCTGAGCGAT 247  
QY 242 TCTCTGGGTCCAAATCAGGGAACACCGCCACCTCAGCATCAACGGGGTCCGAGCGCGG 301  
Db 248 TCTCTGGGTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCAGACCCAGGCTATGG 307  
QY 302 ATGAGGCTGACTATTACTGTAGGTGTGGGACAGGCTAGTGTATCATCCGGTCTTCGGAG 361  
Db 308 ATGAGGCTGACTATTACTGTAGGCTGGGAC-----AGTAACACTGTGTGTCTTCGGCG 361  
QY 362 GAGGACCCGGGTGACCGTCTAGTGTAGCCCAAGGCTGCCCTCGGTCACTCTGTTC 421  
Db 362 GAGGACCAAGCTGACCGTCTAGTGTAGCCCAAGGCTGCCCTCGGTCACTCTGTTC 421  
QY 422 CGCCCTCTCTCAGGAGCTTCAAGCCCAAGGCCACACTGTGTGTCTCTATAAGTGACT 481  
Db 422 CGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCACACTGTGTGTCTCTATAAGTGACT 481  
QY 482 TCTACCCGGGAGCCGTGACAGTGGCTGGAAGGAGATAGCAGCCCCCTCAAGGGGGAG 541  
Db 482 TCTACCCGGGAGCCGTGACAGTGGCTGGAAGGAGATAGCAGCCCCCTCAAGGGGGAG 541  
QY 542 TGGAGACACACACACCTCCAAACAAAGCAACAAAGTACGGGGCCAGCGTACTCTCA 601  
Db 542 TGGAGACACACACACCTCCAAACAAAGCAACAAAGTACGGGGCCAGCGTACTCTCA 601  
QY 602 GCTGACGCTGAGCAGTGGAAAGTCCACAGAAAGCTACAGTCCAGGTCACGCATGAAG 661  
Db 602 GCTGACGCTGAGCAGTGGAAAGTCCACAGAAAGCTACAGTCCAGGTCACGCATGAAG 661  
QY 662 GGAGCACCGTGGAGAGACAGTGGCCCTTACAGATGTTTCAT 703  
Db 662 GGAGCACCGTGGAGAGACAGTGGCCCTTACAGATGTTTCAT 703

RESULT 15

AAS22777  
ID AAS22777 standard; cDNA; 1825 BP.  
XX  
AC AAS22777;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Human cDNA encoding a novel human protein #343.

XX Human; novel protein; ss; Antianaemic; osteopathic; antiinflammatory;  
KW immunomodulatory; cytosolic; neuroprotective; vulnery; nootropic;  
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;  
KW antibacterial; antiallergic; dermatological; haemostatic; antiashtatic;  
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;  
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
KW tissue regeneration; immune disorder.

OS Homo sapiens.

XX WO200155437-A2.

PN 02-AUG-2001.

PD 25-JAN-2001; 2001WO-US02623.

XX



PR 25-JAN-2000; 2000US-0491404.  
XX (HYSE-) HYSEQ INC.  
PA  
XX Tang YT, Liu C, Drmanac RT;  
PI  
XX WPI; 2001-451939/48.  
DR P-PSDB; ANU14472.  
DR  
XX  
PT Isolated polypeptides useful for treating anti-inflammatory diseases,  
PT nervous system disorders, and for regenerating bone and cartilage -  
XX  
XX Claim 1; Page 721-722; 894pp; English.  
XX  
CC The invention relates to polynucleotides encoding novel human  
CC proteins or their active domains. The polypeptides, polynucleotides and  
CC antibodies raised against the polypeptides are used in a method of  
CC treatment of a mammal and prevention of disorders caused by the aberrant  
CC protein expression or activity. The polypeptides can be used as  
CC molecular weight markers, food supplements, and in antibody production.  
CC The polypeptides are used to identify compounds which bind to the  
CC polypeptides. Polynucleotides of the invention are used as probes and  
CC primers, for sequencing, for chromosome or gene mapping, in the  
CC production of recombinant proteins, and in generating anti-sense DNA or  
CC RNA and in gene therapy. Polypeptides of the invention can be used to  
CC target drugs to a tumour, in assays to determine biological activity, to  
CC raise antibodies/ elicit an immune response, to determine quantitative  
CC protein levels, as tissue markers, and to isolate receptors or ligands.  
CC Polypeptides of the invention may also be useful in treating platelet  
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
CC the proliferation, differentiation and survival of stem cells, as a  
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
CC fungal infection or from autoimmunity, cancer, allergy, asthma,  
CC graft-versus-host disease, eczema, haemophilia, thrombosis,  
CC anti-inflammatory diseases, nervous system disorders, and infection.  
CC The present sequence encodes a protein of the invention.  
XX  
SQ Sequence 1825 BP; 361 A; 509 C; 560 G; 395 T; 0 other;  
Query Match 73.0%; Score 515, DB 22; Length 1825;  
Best Local Similarity 87.4%; Pred. NO. 2e-119;  
Matches 576; Conservative 0; Mismatches 80; Indels 3; Gaps 1;  
QY 45 CCCAGGTGCACGATGTCCTATGAACCTCAGCCACCCCTCGGTGCTAGTGTCCTCCAGG 104  
DB 73 CACAGGGCCGTGGCCCTCTATGAGCTGACTCAGCCACCCCTCAGTGCTCGTGTCCAGG 132  
QY 105 ACAGAGCCGACGATCACCCTGTGGGGAGACACACAGTAGAAATGATATGTCCACTGGTA 164  
DB 133 ACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGATAAAATTGCTTGCTGTA 192  
QY 165 CCAGCAGAGCCAGCGGGCCCTTACTGTGCTATCTATGATAGTAGCAGCGCCCTC 224  
DB 193 TCAGGTGAAGCCAGGCCAGTCCCTTTAGTGGTCTCATCAAGATACCAAGCGGCCCTC 252  
QY 225 AGGGATCCCTGAGCGGATCTCTGGCTCCAAATCAGGGACACGCCACCCCTGACCATCAA 284  
DB 253 AGGGATCCCTGAGCGGATCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAG 312  
QY 285 CGGGGTTCAGAGCCGGGGATGAGGCTGACTATTACTGTCTAGGTGTGGGACAGGGCTAGTGA 344  
DB 313 CGGGACCCAGGCTATGATGAGGCTGACTATTACTGTCTAGGCGTGGACAG---CAGCTC 369  
QY 345 TCATCCGGTCTTCGGAGGAGGACCCGGGTGACCGGTCTTAGGTACGCCCAAGGCTGCCCC 404  
DB 370 TTATGTGGCGTTTCGGCGGAGGGACCAAGCTGACCCGCTCTAGGTACGCCCAAGGCTGCCCC 429  
QY 405 CTCGGTCACTCTGTTCCTCCGCTCTCTCTGAGGAGCTTCAAGCCACAGGCCACACTGGT 464  
DB 430 CTCGGTCACTCTGTTCCTCCGCTCTCTCTGAGGAGCTTCAAGCCACAGGCCACACTGGT 489

QY 465 GTGTCTCATAGTGAATCTTACCCGGGAGCCCTGTGACAGTGGGCTGGAAGGACATAGCAG 524  
DB 490 GTGTCTCATAGTGAATCTTACCCGGGAGTCCGTGACAGTGGGCTGGAAGGACATAGCAG 549  
QY 525 CCCCGTCAAGCGGGGAGTGGAGACACACACCCCTCCAAACAAAGCAACAAAGTACGC 584  
DB 550 CCCCGTCAAGCGGGGAGTGGAGACACACACCCCTCCAAACAAAGCAACAAAGTACGC 609  
QY 585 GGCCAGCAGCTACCTGAGCCTTGACGCTGAGCAGTGGAGTCCCAAGAGCTTACAGCTG 644  
DB 610 GGTGAGCAGCTATCTGAGCCTGACGCTGAGCAGTGGAGTCCCAAGAGCTTACAGCTG 669  
QY 645 CCAGGTACGCATGAAGGAGCACCGTGGAGAGACAGTGGGCCCCCTTACAGAAATGTTTCA 703  
DB 670 CCAGGTACGCATGAAGGAGCACCGTGGAGAGACAGTGGGCCCCCTTACAGAAATATTTAT 728  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
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Perfect score: 705

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Scoring table:

IDENTITY NUC

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Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*

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13: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
14: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	705	100.0	705	US-10-124-905-1	Sequence 1, Appli
2	705	100.0	705	US-09-948-429B-1	Sequence 1, Appli
3	705	100.0	705	US-10-073-138-1	Sequence 1, Appli
4	585.2	83.0	702	US-10-211-357-5	Sequence 5, Appli
5	540.2	76.6	711	US-10-124-905-9	Sequence 9, Appli
6	540.2	76.6	711	US-09-948-429B-9	Sequence 9, Appli
7	540.2	76.6	711	US-10-073-138-5	Sequence 5, Appli
8	530	75.2	868	US-09-822-849A-157	Sequence 157, App
9	512.8	72.7	960	US-09-925-301-582	Sequence 582, App
10	510.6	72.4	2667	US-10-158-646-76	Sequence 76, Appli
11	501.6	71.1	830	US-09-981-353-42	Sequence 42, Appli
12	488.6	69.3	846	US-09-981-353-55	Sequence 55, Appli
13	487	69.1	1480	US-09-981-353-146	Sequence 146, App
14	473.8	67.2	857	US-09-822-849A-158	Sequence 158, App
15	472	67.0	768	US-09-747-669-4	Sequence 4, Appli
16	472	67.0	768	US-09-747-669-5	Sequence 5, Appli
17	465.6	66.0	826	US-10-098-841-316	Sequence 316, App
18	463.2	65.7	848	US-10-158-646-70	Sequence 70, Appli
19	463	65.7	888	US-10-158-646-71	Sequence 71, Appli

#### ALIGNMENTS

##### RESULT 1

US-10-124-905-1

; Sequence 1, Application US/10124905

; Patent No. US20020166136A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/124,905

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/383,916

; FILING DATE:

; APPLICATION NUMBER: US 08/487,550

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Taskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 705 base pairs

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21	462.8	65.6	915	10	US-09-880-107-3743	Sequence 3743, Ap
22	461.8	65.5	883	9	US-10-158-646-73	Sequence 73, Appl
23	457.2	64.9	670	9	US-09-968-433-40	Sequence 40, Appl
24	449.2	63.7	2667	9	US-10-158-646-76	Sequence 76, Appl
25	447.6	63.5	2112	9	US-10-001-857-108	Sequence 108, App
26	435.6	61.8	885	9	US-09-852-797-47	Sequence 47, Appl
27	435.6	61.8	885	10	US-09-853-161-47	Sequence 47, Appl
28	435.6	61.8	885	10	US-09-852-797-29	Sequence 29, Appl
29	434	61.6	879	9	US-09-852-797-29	Sequence 29, Appl
30	434	61.6	879	10	US-09-853-161-29	Sequence 29, Appl
31	434	61.6	879	10	US-09-852-797-46	Sequence 46, Appl
32	432.2	61.3	928	9	US-09-852-797-46	Sequence 46, Appl
33	432.2	61.3	928	10	US-09-853-161-46	Sequence 46, Appl
34	432.2	61.3	928	10	US-09-852-797-29	Sequence 29, Appl
35	415.4	58.9	1480	9	US-09-981-353-146	Sequence 146, Appl
36	407.4	57.8	579	9	US-10-158-646-75	Sequence 75, Appl
37	395.4	56.1	764	9	US-09-981-353-46	Sequence 46, Appl
38	392.4	55.7	491	9	US-09-736-457-833	Sequence 833, App
39	392.4	55.7	491	9	US-09-902-941-833	Sequence 833, App
40	392.4	55.7	491	9	US-09-849-626-833	Sequence 833, App
41	392.4	55.7	491	9	US-10-017-754-833	Sequence 833, App
42	389.4	55.2	558	9	US-09-920-455-58	Sequence 58, Appl
43	387.4	55.0	608	9	US-09-736-457-908	Sequence 908, App
44	387.4	55.0	608	9	US-09-902-941-908	Sequence 908, App
45	387.4	55.0	608	9	US-09-849-626-908	Sequence 908, App



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QY 361 GGAGGACCCGGGTGACCGTCTAGTGTAGTCCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC 420
D 361 GGAGGACCCGGGTGACCGTCTAGTGTAGTCCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC 420
QY 421 CGGCCCCCTCTCTGAGGAGCTTCAAGGCAACAAGGCCACACTGGTGTCTCTATAAGTGAC 480
D 421 CGGCCCCCTCTCTGAGGAGCTTCAAGGCAACAAGGCCACACTGGTGTCTCTATAAGTGAC 480
QY 481 TTCTACCCGGGACCGCTGACAGTGGCCCTGGAAGGCAAGTACGCGGCCAGAGCTACCTG 600
D 481 TTCTACCCGGGACCGCTGACAGTGGCCCTGGAAGGCAAGTACGCGGCCAGAGCTACCTG 600
QY 541 GTGGAGACCAACACACCCCTCCAAACAAAGCAACAAGTACGCGGCCAGAGCTACCTG 660
D 541 GTGGAGACCAACACACCCCTCCAAACAAAGCAACAAGTACGCGGCCAGAGCTACCTG 660
QY 601 AGCTGACCCCTGAGCAGTGGAGTCCCAAGCAAGCTACAGTGCAGGTCACGATGAA 660
D 601 AGCTGACCCCTGAGCAGTGGAGTCCCAAGCAAGCTACAGTGCAGGTCACGATGAA 660
QY 661 GGGAGCACCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 705
D 661 GGGAGCACCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 705

RESULT 3
US-10-073-138-1
; Sequence 1, Application US/10073138
; Publication No. US20020187146A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, Darrell R.
;           HANNA, Nabil
;           BRAMS, Peter
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
; INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1
; AND B7.2 CO-STIMULATORY ANTIGENS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/073,138
; FILING DATE: 13-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,361
; FILING DATE: 08-NOV-1996
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-073-138-1
Query Match 100.0%; Score 705; DB 9; Length 705;
Best Local Similarity 100.0%; Pred. No. 8.1e-205; Indels 0; Gaps 0;
Matches 705; Conservative 0; Mismatches 0;
QY 1 ATGAGGGTCCCCGGCTCAGCTCCTGGGGCTCTCTGGCTCTGGCTCCAGGTGCACCATGT 60
D 1 ATGAGGGTCCCCGGCTCAGCTCCTGGGGCTCTCTGGCTCTGGCTCCAGGTGCACCATGT 60
QY 61 GCCTATGAATCACTCAGCCACCTCGGTGTCAAGTGTCTCCAGGACAGCGCCAGGATC 120
D 61 GCCTATGAATCACTCAGCCACCTCGGTGTCAAGTGTCTCCAGGACAGCGCCAGGATC 120
QY 121 ACCTGTGGGGAGACAACAGTAGAATGAATATGTCCTGCTACCTGCTACAGCAGAGCCAGCG 180
D 121 ACCTGTGGGGAGACAACAGTAGAATGAATATGTCCTGCTACCTGCTACAGCAGAGCCAGCG 180
QY 181 CGGGCCCCCTATCTGCTCATCTATGATGATAGTACCGGCCCTCAGGGATCCCTGAGCGA 240
D 181 CGGGCCCCCTATCTGCTCATCTATGATGATAGTACCGGCCCTCAGGGATCCCTGAGCGA 240
QY 241 TTCTCTGGCTCCAAATCAGGGAAACACCGCCACCTGACCATCAACGGGGTCGAGGCCGGG 300
D 241 TTCTCTGGCTCCAAATCAGGGAAACACCGCCACCTGACCATCAACGGGGTCGAGGCCGGG 300
QY 301 GATGAGGCTGACTATTACTGTGCTGAGTGGGACAGGGCTAGTGTATCATCCGTTCTTCGGA 360
D 301 GATGAGGCTGACTATTACTGTGCTGAGTGGGACAGGGCTAGTGTATCATCCGTTCTTCGGA 360
QY 361 GGAGGAGCCCGGTGACCGTCTAGTCTAGCCCCAAGGGTGGCCCCCTCGGTCACTCTGTTTC 420
D 361 GGAGGAGCCCGGTGACCGTCTAGTCTAGCCCCAAGGGTGGCCCCCTCGGTCACTCTGTTTC 420
QY 421 CGGCCCCCTCTGAGGAGCTTCAAGCCAAACAAAGCCACACTGGTGTCTCATAAGTGAC 480
D 421 CGGCCCCCTCTGAGGAGCTTCAAGCCAAACAAAGCCACACTGGTGTCTCATAAGTGAC 480
QY 481 TTCTACCCGGGAGCCGTGACAGTGGCTGGAAGGAGAGATAGCAGCCCCCTCAAGGCCGGA 540
D 481 TTCTACCCGGGAGCCGTGACAGTGGCTGGAAGGAGAGATAGCAGCCCCCTCAAGGCCGGA 540
QY 541 GTGGAGACCAACACACCCCTCCAAACAAAGCAACAAGTACGCGGCCAGAGCTACCTG 600
D 541 GTGGAGACCAACACACCCCTCCAAACAAAGCAACAAGTACGCGGCCAGAGCTACCTG 600
QY 601 AGCTGACCCCTGAGCAGTGGAGTCCCAAGCAAGCTACAGTGCAGGTCACGATGAA 660
D 601 AGCTGACCCCTGAGCAGTGGAGTCCCAAGCAAGCTACAGTGCAGGTCACGATGAA 660
QY 661 GGGAGCACCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 705
D 661 GGGAGCACCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 705

RESULT 4
US-10-211-357-5
; Sequence 5, Application US/10211357
; Publication No. US20030077275A1
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
;           Newman, Roland A.
;           Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
```

CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314-3187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICANT: Anderson, Darrell R.  
FILING DATE: 05-Aug-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/612,914A  
FILING DATE: 10-Jul-2000  
APPLICATION NUMBER: US 08/523,894  
FILING DATE: 06-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-165  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 702 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORGANISM: Homo sapiens  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: lambda variable and constant domains in  
CE9.1  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..702  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 1..702  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-211-357-5  
Query Match 83.0%; Score 585.2; DB 9; Length 702;  
Best Local Similarity 89.6%; Pred. No. 2.3e-168;  
Matches 629; Conservative 0; Mismatches 73; Indels 0; Gaps 0;  
QY 4 AGGGTCCCGCTCAGCTCCTGGGGCTCTGCTCTGCTCCAGGTGCACGATGTGC 63  
DB 1 ATGGCTGGGCTCTGCTCTCTCGGCTCTGCTCACTTTACAGACTCTGGGCTCC 60  
QY 64 TATGAATGACTCAGCCACCTCGGTGTAGTGTCCCGAGGACAGCGGCAGGATCAC 123  
DB 61 TATGAGTTGAGTCAGCTCGCTCAGTGTCCGTCCTCCAGGACAGACGGCGGTTCAC 120  
QY 124 TGTGGGGGACACAGTGAATATGTCTCAGTGTCTGCTTACAGCAGAGCAGCGCG 183  
DB 121 TGTGGGGGACACAGTGTGAAGAAAGTGTACAGTGTGTACAGAGGACCGCCAG 180  
QY 184 GCCCTTATCTGCTATCTATGATGATGATGACCGGCTCTCAGGGATCCCTGAGCGATT 243  
DB 181 GCCCTGTGCTGCTATCTATGCTGACAGGACCGGCTCTCAGGGATCCCTGCGGATT 240  
QY 244 TCTGGCTCCAAATCAGGGAACACCGCACCTGACCATCAACCGGGTTCAGGCGCGGGAT 303  
DB 241 TCTGGCTCCAAATCAGGGAACACCGCACCTGACCATCAACCGGGTTCAGGCGCGGGAT 300  
QY 304 GAGGCTGACTATTACTGTAGGTGTGGACAGGGCTAGTATCATCGGTCTTCGAGGA 363  
DB 301 GAGGCTGACTATTACTGTAGGTGTGGACAGGGCTAGTATCATCGGTCTTCGAGGA 360

QY 364 GGGACCCGGGTGACCGTCTAGGTGAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCGG 423  
DB 361 GGGACCCGGGTGACCGTCTAGGTGAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCGG 420  
QY 424 CCCTCTCTGAGGAGCTTCAAGCCCAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 483  
DB 421 CCCTCTCTGAGGAGCTTCAAGCCCAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 480  
QY 484 TACCCGGGAGCGGTGACAGTGGCTGGAAGGAGGAGTACAGCCCGCTCAAGGCGGAGTG 543  
DB 481 TACCCGGGAGCGGTGACAGTGGCTGGAAGGAGGAGTACAGCCCGCTCAAGGCGGAGTG 540  
QY 544 GAGACCAACACACCTCCCAACAAAGCAACAAAGTACGCGGCGAGGCTACCTGAGC 603  
DB 541 GAGACCAACACACCTCCCAACAAAGCAACAAAGTACGCGGCGAGGCTACCTGAGC 600  
QY 604 CTGAGCGCTGAGCAGTGGAGTCCCAAGGAGTACAGGCTGAGGCTGAGGCTGAGGCTGAG 663  
DB 601 CTGAGCGCTGAGCAGTGGAGTCCCAAGGAGTACAGGCTGAGGCTGAGGCTGAGGCTGAG 660  
QY 664 AGCAGCGTGGAGAGACAGTGGCGCTTACAGATGTTATGA 705  
DB 661 AGCAGCGTGGAGAGACAGTGGCGCTTACAGATGTTATGA 702  
RESULT 5  
US-10-124-905-9  
Sequence 9, Application US/10124905  
Patent No. US2002016136A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
TITLE OF INVENTION: IMMUNOSUPPRESSANTS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/124,905  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/383,916  
FILING DATE:  
APPLICATION NUMBER: US 08/487,550  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:

NAME/KEY: CDS  
LOCATION: 1..711  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 1..711  
US-10-124-905-9

Query Match 76.6%; Score 540.2; DB 9; Length 711;  
Best Local Similarity 86.1%; Pred. No. 1.1e-154;  
Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;  
QY 1 ATGAGGGTCCCGCTCAGCTCTGGGGCTCTGCTCTGGCTCCAGGTGACCATGT 60  
DB 1 ATGAGGGTCCCGCTCAGCTCTGGGGCTCTGCTCTGGCTCCAGGTGACCATGT 60  
QY 61 GCCTATGAATGACTCAGCCACCTCGGTGTCTAGTGTCCCGAGGAGGAGGATC 120  
DB 61 GAGTCTGTCTGACACAGCGGCTCAGTGTCTGGGGCTCCAGGTGACCATGT 120  
QY 121 ACTGTGGGGG-----AGACAACAGTAGAATGATATGTCACGTGGTACGAGAG 174  
DB 121 TGTGTGACTGGGAGGACCTCCAACTTGGAGGTATGATCTACATTTGGTACGAGCTC 180  
QY 175 CCAGCGCGGGCCCTATCTGCTATGATGATAGTACCGGCTCCAGGATCCCT 234  
DB 181 CCAGGAAACGGCCCCAACTCTCTATGATGATGATGATGATGATGATGATGAT 240  
QY 235 GAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCGAG 294  
DB 241 GACCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCGAG 300  
QY 295 GCCGGGATGAGGCTGATCTATCTGTCAGGTGTGGGAGAGGGCTAGTATCATCCGGTC 354  
DB 301 ACTGAGGATGAGGCTGATCTATCTGTCAGGTGTGGGAGAGGGCTAGTATCATCCGGTC 360  
QY 355 TTCCGAGGAGGACCGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 414  
DB 361 TTCCGAGGAGGACCGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
QY 415 CTGTTCCCGCTCTCTGAGGAGCTTCAAGCAACAGGCAACAGGCTGCTGCTGCTGCTGCT 474  
DB 421 CTGTTCCCGCTCTCTGAGGAGCTTCAAGCAACAGGCAACAGGCTGCTGCTGCTGCTGCT 480  
QY 475 AGTGAATTTACCGGGAGCGGTGACAGTGGCTGGAAGGAGATGAGCCCGCTCAAG 534  
DB 481 AGTGAATTTACCGGGAGCGGTGACAGTGGCTGGAAGGAGATGAGCCCGCTCAAG 540  
QY 535 GCGGGAGTGGAGACCAACACCTCCAAACAAAGCAACAGGATGAGGAGGAGGAGGAGGAG 594  
DB 541 GCGGGAGTGGAGACCAACACCTCCAAACAAAGCAACAGGATGAGGAGGAGGAGGAGGAG 600  
QY 595 TACCTGAGCTGACGCTGAGCAGTGGAGTCCAGAGGCTTACAGCTGCGCAGGTCAAG 654  
DB 601 TACCTGAGCTGACGCTGAGCAGTGGAGTCCAGAGGCTTACAGCTGCGCAGGTCAAG 660  
QY 655 CATGAAGGAGGACCGTGGAGAGAGCAGTGGGCTTACAGATGTTTCATGA 705  
DB 661 CATGAAGGAGGACCGTGGAGAGAGCAGTGGGCTTACAGATGTTTCATGA 711

## RESULT 6

US-09-948-429B-9  
Sequence 9, Application US/09948429B  
Patent No. US20020177689A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
TITLE OF INVENTION: IMMUNOSUPPRESSANTS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/948,429B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/383,916  
FILING DATE:  
APPLICATION NUMBER: US 08/487,550  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..711  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 1..711  
US-09-948-429B-9

Query Match 76.6%; Score 540.2; DB 9; Length 711;  
Best Local Similarity 86.1%; Pred. No. 1.1e-154;  
Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;  
QY 1 ATGAGGGTCCCGCTCAGCTCTGGGGCTCTGCTCTGGCTCCAGGTGACCATGT 60  
DB 1 ATGAGGGTCCCGCTCAGCTCTGGGGCTCTGCTCTGGCTCCAGGTGACCATGT 60  
QY 61 GCCTATGAATGACTCAGCCACCTCGGTGTCTCCCGAGGAGGAGGATC 120  
DB 61 GAGTCTGTCTGACACAGCGGCTCAGTGTCTGGGGCTCCAGGTGACCATGT 120  
QY 121 ACTGTGGGGG-----AGACAACAGTAGAATGATATGTCACGTGGTACGAGAG 174  
DB 121 TGTGTGACTGGGAGGACCTCCAACTTGGAGGTATGATCTACATTTGGTACGAGCTC 180  
QY 175 CCAGCGCGGGCCCTATCTGCTATGATGATAGTACCGGCTCCAGGATCCCT 234  
DB 181 CCAGGAAACGGCCCCAACTCTCTATGATGATGATGATGATGATGATGATGAT 240  
QY 235 GAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCGAG 294  
DB 241 GACCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCGAG 300  
QY 295 GCCGGGATGAGGCTGATCTATCTGTCAGGTGTGGGAGAGGGCTAGTATCATCCGGTC 354  
DB 301 ACTGAGGATGAGGCTGATCTATCTGTCAGGTGTGGGAGAGGGCTAGTATCATCCGGTC 360  
QY 355 TTCCGAGGAGGACCGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 414  
DB 361 TTCCGAGGAGGACCGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

415	Qy	CTGTTC	CCGCCCTCCTCTGAGAGCTTCAAGCCAAACAGGCCACACTGTGTGTCTCATATA	474
421	Db	CTGTTC	CCGCCCTCCTCTGAGAGCTTCAAGCCAAACAGGCCACACTGTGTGTCTCATATA	480
475	Qy	AGTGACTTCTAC	CCGGGAGCGGTGACAGTGGCCCTGGAAAGCAGATAGCAGCCCCGCTCAAG	534
481	Db	AGTGACTTCTAC	CCGGGAGCGGTGACAGTGGCCCTGGAAAGCAGATAGCAGCCCCGCTCAAG	540
535	Qy	GCGGAGTGGAGAC	CAACCACTCTCCAAACAAAGCAACCAAGTACGGCGCCAGCAGC	594
541	Db	GCGGAGTGGAGAC	CAACCACTCTCCAAACAAAGCAACCAAGTACGGCGCCAGCAGC	600
595	Qy	TACCTGAGCCTCAG	CCGCTGACGAGTGGAAAGTCCACACAGAAGCTACAGTGCSCAGGTTCAGC	654
601	Db	TACCTGAGCCTCAG	CCGCTGACGAGTGGAAAGTCCACACAGAAGCTACAGTGCSCAGGTTCAGC	660
655	Qy	CATGAAGGGGAGC	ACCGTGGGAGAGCAGTGGCCCCCTACAGAAATGTTTCATGA	705
661	Db	CATGAAGGGGAGC	ACCGTGGGAGAGCAGTGGCCCCCTACAGAAATGTTTCATGA	711

## RESULT 7

```

US-10-073-138-5
; Sequence 5, Application US/10073138
; Publication No. US20020187146A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, Darrell R.
; HANNA, Nabil
; BRAMS, Peter
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
; INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1
; AND B7.2 CO-STIMULATORY ANTIGENS
;

```

Query Match	76.6%	Score 540.2	DB 9	Length 711		
Best Local Similarity	86.1%	Prod. No. 1.1e-154				
Matches 612	Conservative 0	Mismatches 93	Indels 6	Gaps 1		
QY	1	ATGAGGTC	CCCGCTCAGCTC	CTGGGGCTCCTGCTCTTGGCTCC	CAGGTGCAGATGT 60	
DB	1	ATGAGGTC	CCCGCTCAGCTC	CTGGGGCTCCTGCTCTTGGCTCC	CAGGTGCAGATGT 60	
QY	61	GCCTATGA	CTGACTCAGCC	CACCTCGGTGTCA	GTTCCTCCAGGACAGCCGAGGATC 120	
DB	61	GAGTGTGT	CTGACACAGCC	CCCTCAGTGTCTTGGGGCC	CCAGGGCAGAAGGTCAACATC 120	
QY	121	ACCTGTGGGG	-----	AGACACAGTAGA	AAATGAATATGTCACTGGTAC	CAGCAGANG 174
DB	121	TCGTGCA	CTGGGACCTCCA	CAATTGGAGGTATGATCTA	CATTGGTAC	CAGCAGCTC 180
QY	175	CCAGCGGG	CCCCCTATAC	TGGTTCATCTATGATGAT	GTACACCGGCCCTCAGGGATCCCT 234	
DB	181	CCAGGA	ACGGCCCCAA	CTCTCATCTATGA	CATTAAAGCGACCTTCAGGAATTTCT 240	
QY	235	GAGCGATT	CTCTGGCTCCA	AAATCAGGAA	CACCGCCACCTCTGACCATCAACGGGGTCGAG 294	
DB	241	GACCGATT	CTCTGGCTCCA	AGTCTGGTACCGCGGCTCCT	TGGCCATCACTGGGCTCCAG 300	
QY	295	GCGGGG	ANGAGGTGATTA	TACTATCTAGGTGTGG	ACAGGGCTAGTGATCATCGGTC 354	
DB	301	ACTGAG	TAGGCTGATTATTA	TCTGTCAGTCTTATGAC	AGCAGCCTGAATGCTCAGGTA 360	
QY	355	TTCCGGAG	GGGACCCGGGTG	ACCGTCTTAGGTACGCC	CAAGGCTGCCCCCTCGGTCACT 414	
DB	361	TTCCGGAG	GGGACCCGGGTG	ACCGTCTTAGGTACGCC	CAAGGCTGCCCCCTCGGTCACT 420	
QY	415	CTGTTCCG	CCCTCCTCTGAG	GAGCTTTCAAGCC	CAACAGGCCACACTGGTGTGTCTCAT 474	
DB	421	CTGTTCCG	CCCTCCTCTGAG	GAGCTTTCAAGCC	CAACAGGCCACACTGGTGTGTCTCAT 480	
QY	475	AGTGATCT	TACCCGGAGCGGTG	ACGTGGCTTGG	AAGCGCAGATAGACGCCCTCGTCAAG 534	
DB	481	AGTGACT	TTTACCCGGAGCGGTG	ACGTGGCTTGG	AAGCGCAGATAGACGCCCTCGTCAAG 540	
QY	535	GCGGAG	TGGAGACCA	CACACCTCCAA	CAAAAGCAACAAGGTACGCGGCACGACG 594	
DB	541	GCGGAG	TGGAGACCA	CACACCTCCAA	CAAAAGCAACAAGGTACGCGGCACGACG 600	
QY	595	TACCTG	AGCTTGACGTG	GGAAGTCC	CAAGAAGCTTACAGCTGCCAGGTCAAG 654	
DB	601	TACCTG	AGCTTGACGTG	GGAAGTCC	CAAGAAGCTTACAGCTGCCAGGTCAAG 660	
QY	655	CATGAG	GGGACACCGTGG	AGAGACAGTGG	CCCTCTACAGATGTTTCATGA 705	
DB	661	CATGAG	GGGACACCGTGG	AGAGACAGTGG	CCCTCTACAGATGTTTCATGA 711	

## RESULT 8

KES001: 8  
 ; Sequence 157, Application US/09822849A  
 ; Patent No. US20020045170A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wong, Gordon G.  
 ; APPLICANT: Clark, Hilary  
 ; APPLICANT: Fechtel, Kim  
 ; APPLICANT: Agostino, Michael J.  
 ; APPLICANT: Howes, Steven H.  
 ; APPLICANT: Reenick, Richard J.  
 ; APPLICANT: Gulukota, Kamalakara  
 ; APPLICANT: Graham, James R.  
 ; APPLICANT: Genetics Institute, Inc.  
 ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
 ; FILE REFERENCE: GIN 6403  
 ; CURRENT APPLICATION NUMBER: US/09/822,849A  
 ; CURRENT FILING DATE: 2001-09-04  
 ; PRIOR APPLICATION NUMBER: 60/195,582







[illegible]

RESULT 14  
US-09-822-849A-158  
; Sequence 158, Application US/09822849A  
; Patent No. US20020045170A1  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fecthel, Kim  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Howes, Steven H.  
; APPLICANT: Resnick, Richard J.  
; APPLICANT: Gulukota, Kamalakara  
; APPLICANT: Graham, James R.  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
; FILE REFERENCE: GIN 6403  
; CURRENT APPLICATION NUMBER: US/09/822,849A  
; CURRENT FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 60/195,582  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 598  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 158  
; LENGTH: 857  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-822-849A-158

Query Match 67.2%; Score 473.8; DB 10; Length 857;  
Best Local Similarity 83.3%; Pred. No. 1.9e-134;  
Matches 554; Conservative 0; Mismatches 102; Indels 9; Gaps 1;

QY 48 AGGTGACGATGTCCTATGAACTGACCTAGCCACCTCGGTCTCAGTGTCCCGACGACA 107  
DB 54 AGTTCTGTGGTTCTTCTGAGCTGACTCAGGACCTGTGTCTGTGGCCCTGGGACA 113  
QY 108 GACGGCCAGGATCACCTGTGGGGAGACACAGTAGAAATGAATATGTCACCTGGTACCA 167  
DB 114 GACAGTCAGGATCACATGCCGAGGAGACACCTCGGAAAGTATTATACAAATTTGGTACCA 173  
QY 168 GCAGAGCCAGCGGGGGCCCTTACTGTGTCATCTATGATGATA-----GTACCG 218  
DB 174 ACTGAAGCCAGGACAGCGCCCTCTCTGTGTGTCATGTTGTAATAAACAACCGCACACCG 233  
QY 219 GCCTCAGGAGTCCCTGAGCGATTCTCTGGCTCCAAATCAGGAACACCGCCACCTGTAC 278  
DB 234 GCCTCAGGAATCCCAGAACGATTCTCTGGCTCCATCTCAGGAACACAGCTTCCCTTGAC 293  
QY 279 CATCAACGGGGTCCAGGCCGGGATGAGGCTGACTATTACTGTGTCAGGTGTGGACAGGGC 338  
DB 294 CATCACTGGGGCTCAGGTTGAAGTAGTCTGACTTTTACTGTAGTTCCCGGACAGCAG 353  
QY 339 TAGTGATCATCCCGTCTTCGGAGAGGACCCCGGTGACCGTCTTAGGTGAGCCCAAGGC 398  
DB 354 TGGTAAAAATTGGGTGTTCGGCGGTGGGACCAAGCTGACCGTCTTAAGTCAGGCCAAGGC 413  
QY 399 TGCCCTCGTCTGCTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCAC 458  
DB 414 TGCCCTCGTCTGCTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCAC 473  
QY 459 ACTGGTGTGTCTCATAGTACTTCTACCCGGGAGCGGTGACAGTGGCCCTGGAAGGCAGA 518  
DB 474 ACTGGTGTGTCTCATAGTACTTCTACCCGGGAGCGGTGACAGTGGCCCTGGAAGGCAGA 533  
QY 519 TAGCAGCCCGTCAAGCGGAGGTGGAGACCAACACCCCTCCAAACAAAGCAACAA 578  
DB 534 TAGCAGCCCGTCAAGCGGAGGTGGAGACCAACACCCCTCCAAACAAAGCAACAA 593  
QY 579 GTACGGGGCAGCAGTACCTGAGCCTGAGCGCTGAGCAGTGAAGTCCACAGAGCTA 638  
DB 594 GTACGGGGCAGCAGTACCTGAGCCTGAGCGCTGAGCAGTGAAGTCCACAAAGCTA 653

QY 639 CAGCTGCCAGGTACGCATGAAGGAGGACACCTGGAGAGACAGTGGCCCTACAGAATG 698  
DB 654 CAGCTGCCAGGTACGCATGAAGGAGGACACCTGGAGAGACAGTGGCCCTACAGAATG 713  
QY 699 TTCAT 703  
DB 714 TTCAT 718

RESULT 15  
US-09-747-669-4  
; Sequence 4, Application US/09747669  
; Patent No. US20020122807A1  
; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.  
; APPLICANT: Saleh, Mansoor  
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED  
; TITLE OF INVENTION: 4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES  
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS  
; TITLE OF INVENTION: AND DETECTION OF CANCERS  
; FILE REFERENCE: 316082001001  
; CURRENT APPLICATION NUMBER: US/09/747,669  
; CURRENT FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: US 09/111,286  
; PRIOR FILING DATE: 1998-07-07  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 768  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-09-747-669-4

Query Match 67.0%; Score 472; DB 10; Length 768;  
Best Local Similarity 84.4%; Pred. No. 6.5e-134;  
Matches 545; Conservative 0; Mismatches 95; Indels 6; Gaps 1;

QY 64 TATGAACGTACCTCAGCCACCTCGGTGTCAGTGTCCCGGAGGACAGCGCCAGGATCAC 123  
DB 79 TCTGTGCTGACTCAGCCACCTCAGCGTCTGGGACCCCGGAGGAGGTACCACTCTCT 138  
QY 124 TGTGGGGAGAGCAACAGTA-----GAAATGAATATGTCCACTGTGTACAGAGAGCCA 177  
DB 139 TGTCTTGAAGCACTCCAAATCAGGAAGTAAAGTGTAACTGTGTACAGCAACTCCCA 198  
QY 178 GCGGGGGCCCTATATCTGTGTATCTATGATGATGATGATGATGATGATGATGATGAT 237  
DB 199 GGAACGGGGCCCAAAATTTCTCATCTATAGTAATAATCAGCGCCCTCAGGGGTCCCTGAC 258  
QY 238 CGATTCTCTGGTCCAAATCAGGAACACCGCCACCTGACCATCAACCGGGTCCAGGGCC 297  
DB 259 CGATTCTCTGGTCCAAAGTCTGGCACCTCAGCTCCCTGGCCATCAGTGGGTCCAGTCT 318  
QY 298 GGGGATGAGCGCTGACTATTACTGTGAGGTGTGGGACAGGGCTAGTGTATCATCCGGTCTTC 357  
DB 319 GAGGATGAGCGTGAATTTACTGTGAGCATGGGATGAGCATGATGATGATGATGATGATGAT 378  
QY 358 GGAGGAGGACCCGGGTGACCGTCTTAGGTGAGCCCAAGGCTGCCCCCTCGGTCACTCTG 417  
DB 379 GCGGAGGAGCAACAGCTGACCGTCTCTGGGTGAGCCCAAGGCTGCCCCCTCGGTCACTCTG 438  
QY 418 TTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAACAGGGCCACACTGTGTGTCTCATAGT 477  
DB 439 TTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAACAGGGCCACACTGTGTGTGTCTCATAGT 498  
QY 478 GACTTCTACCCGGGAGCCGTGACAGTGGCTCTGAAAGGAGATAGACAGCCCGCTCAAGGCG 537  
DB 499 GACTTCTACCCGGGAGCCGTGACAGTGGCTCTGAAAGGAGATAGACAGCCCGCTCAAGGCG 558  
QY 538 GGAGTGGAGACCAACCAACCCCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCTAC 597

Db	559	GGAGTGGAGACCAACACCCCTCCAAACAAAGCAACAAGTACCGGCCAGCAGCTAC	618
Qy	598	CTGAGCCTGACGCTGAGCAGTGGAAAGTCCACAGAAAGCTACAGCTGCCAGGTCAAGCAT	657
Db	619	CTGAGCCTGACGCTGAGCAGTGGAAAGTCCACAGAAAGCTACAGCTGCCAGGTCAAGCAT	678
Qy	658	GAAGGGAGCACCGTGGAGAAAGACAGTGGCCCCCTACAGAATGTTTCAT	703
Db	679	GAAGGGAGCACCGTGGAGAAAGACAGTGGCCCCCTACAGAATGTTTCAT	724

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Job time : 95.9453 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 14:26:38 ; Search time 40.2104 Seconds  
(without alignments)  
5376.898 Million cell updates/sec

Title: US-09-576-424-1  
Perfect score: 705  
Sequence: 1 atgagggtccccctcagct.....ccccctacagaatgttcata 705

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/prodata/1/ina/5A COMB.seq.\*  
2: /cgn2\_6/prodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/prodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/PCUTUS COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	705	100.0	705	3	US-08-487-550-1
2	585.2	83.0	702	3	US-08-523-894-5
3	540.2	76.6	711	3	US-08-487-550-9
4	473	67.1	935	3	US-09-049-672A-20
5	457	64.8	902	2	US-08-378-939-11
6	456	64.7	895	3	US-09-049-672A-25
7	455.4	64.6	891	3	US-09-049-672A-23
8	435.6	61.8	885	4	US-09-152-060-47
9	434	61.6	879	4	US-09-152-060-29
10	432.2	61.3	928	4	US-09-152-060-46
11	425.4	60.3	919	3	US-09-049-672A-24
12	407.4	57.8	716	4	US-08-793-450-5
13	306.6	43.5	584	4	US-09-404-879A-268
14	273.2	38.8	771	4	US-08-991-789A-241
15	273.2	38.8	771	4	US-09-062-451-241
16	273.2	38.8	771	4	US-09-598-326-241
17	267.2	37.9	387	1	US-08-379-072A-20
18	267.2	37.9	387	1	US-08-478-039-109
19	267.2	37.9	387	1	US-08-481-869-20
20	267.2	37.9	387	1	US-08-476-349A-109
21	267.2	37.9	387	1	US-08-476-237-16
22	267.2	37.9	387	3	US-08-523-894-3
23	260.4	36.9	327	4	US-09-202-181-1
24	259.4	36.8	408	4	US-09-025-769B-169
25	249.8	35.4	642	2	US-08-634-783A-4
26	249.8	35.4	642	3	US-09-070-817-4
27	246.2	34.9	346	2	US-08-761-277A-50

Query Match 100.0% ; Score 705 ; DB 3 ; Length 705 ;

ALIGNMENTS

RESULT 1  
US-08-487-550-1  
; Sequence 1, Application US/08487550  
; Patent No. 6113898  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,550  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 705 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..705  
; FEATURE:  
; NAME/KEY: mat peptide  
; LOCATION: 1..705  
US-08-487-550-1

28	246	34.9	333	2	US-08-477-553A-44	Sequence 44, Appl
29	244.2	34.6	324	1	US-08-259-372A-9	Sequence 9, Appl
30	244.2	34.6	324	1	US-08-468-671-9	Sequence 9, Appl
31	242.4	34.4	318	2	US-08-646-981-4	Sequence 4, Appl
32	237.4	33.7	431	2	US-08-345-321-7	Sequence 7, Appl
33	226.4	32.1	318	1	US-08-436-463-9	Sequence 9, Appl
34	226.4	32.1	318	1	US-08-024-253-9	Sequence 9, Appl
35	212	30.1	324	1	US-08-360-123-10	Sequence 10, Appl
36	212	30.1	324	2	US-08-450-578-10	Sequence 10, Appl
37	212	30.1	324	2	US-09-017-628-10	Sequence 10, Appl
38	212	30.1	324	2	US-09-014-880-10	Sequence 10, Appl
39	212	30.1	324	4	US-08-450-363-10	Sequence 10, Appl
40	202.2	28.7	314	4	US-09-370-838-13	Sequence 13, Appl
41	200.2	28.4	831	4	US-09-260-527-2	Sequence 2, Appl
42	200.2	28.4	840	4	US-09-260-527-4	Sequence 4, Appl
43	199.4	28.3	930	4	US-09-079-029-6	Sequence 6, Appl
44	199.4	28.3	939	4	US-09-079-029-7	Sequence 7, Appl
45	187.6	26.6	318	1	US-08-259-372A-15	Sequence 15, Appl





QY 544 GAGACACACACACCTCCAAACAAAGCAACAAAGTACGGCCAGCAGCTACCTGAGC 603  
Db 541 GAGACACACACACCTCCAAACAAAGCAACAAAGTACGGCCAGCAGCTACCTGAGC 600  
QY 604 CTGACCCCTGAGCAGTGGAGTCCCAAGAGCTACAGCTGCCAGGTCAAGCAAGG 663  
Db 601 CTGACCCCTGAGCAGTGGAGTCCCAAGAGCTACAGCTGCCAGGTCAAGCAAGG 660  
QY 664 AGCACCGTGGAGAGACAGTGGCCCTACAGATGTTTCATGA 705  
Db 661 AGCACCGTGGAGAGACAGTGGCCCTACAGATGTTTCATGA 702

RESULT 3  
US-08-487-550-9  
; Sequence 9, Application US/08487550  
; Patent No. 6113898  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,550  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 711 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..711  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 1..711  
US-08-487-550-9

Query Match 76.6%; Score 540.2; DB 3; Length 711;  
Best Local Similarity 86.1%; Pred. No. 1.5e-140;  
Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;

QY 1 ATGAGGTCCTCCCTCAGCTCCCTGGGCTCTCTGCTCTGCTCCAGTCCAGTGCATGT 60  
Db 1 ATGAGGTCCTCCCTCAGCTCCCTGGGCTCTCTGCTCTGCTCCAGTCCAGTGCATGT 60  
QY 61 GCCTATGACTGACTAGCCACCTCGGTGTAGTGTCCCGAGCAGAGCGGCAGATC 120  
Db 61 GAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCCCAGGGAGAGGTCAACATC 120

QY 121 ACCTGTGGGG-----AGACAAACAGTAGAAATGATATGTCCACTGGTACCAGCAGAAG 174  
Db 121 TCGTGCACTGGGAGCAGCTCCCAACATTTGGAGGTATGATCTACTATTGGTACCAGCAGCTC 180  
QY 175 CCAGCGGGGGCCCTTACTGTCTATGTATGATGATGACCGGCCCTCAGGATCCCT 234  
Db 181 CCAGAAACGGGGCCCCAACTCTCTATGATCAATTAACAAAGCAACCTTCAGAAATTTCT 240  
QY 235 GAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACCGGGGTCCAG 294  
Db 241 GACCGATTCTCTGGCTCCAAATCTGGTACCGGGCTCTCTGGCCATCACTGGGCTCCAG 300  
QY 295 GCCGGGATGAGGCTGACTATTCTGTCTAGGTGTGGACAGAGGCTAGTGTATCATCCGGTC 354  
Db 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCGCTGAATGCTCAGGTA 360  
QY 355 TTCCGAGGAGGAGCCCGGTGACCTCTAGGTGACGCCCAAGGCTGCCCTCGGTCACT 414  
Db 361 TTCCGAGGAGGAGCCCGGTGACCTCTAGGTGACGCCCAAGGCTGCCCTCGGTCACT 420  
QY 415 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCAACAAAGCCACACTGGTGTCTCATA 474  
Db 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCAACAAAGCCACACTGGTGTCTCATA 480  
QY 475 ACTGACTTCTACCCGGGAGCCGTGACAGTGGCTGGAAGCAGATAGCAGCCCGTCAAG 534  
Db 481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCTGGAAGCAGATAGCAGCCCGTCAAG 540  
QY 535 GCGGAGTGGAGACCAACACCTCTCAAGCAACAAAGCAACAAAGTACCGGCCAGCAGC 594  
Db 541 GCGGAGTGGAGACCAACACCTCTCAAGCAACAAAGCAACAAAGTACCGGCCAGCAGC 600  
QY 595 TACCTGAGCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTTACAGTGCAGGTCACG 654  
Db 601 TACCTGAGCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTTACAGTGCAGGTCACG 660  
QY 655 CATGAAGGAGCAGCCGTGGAGAGACAGTGGGCCCTTACAGAATGTTTCATGA 705  
Db 661 CATGAAGGAGCAGCCGTGGAGAGACAGTGGGCCCTTACAGAATGTTTCATGA 711

RESULT 4  
US-09-049-672A-20  
; Sequence 20, Application US/09049672A.  
; Patent No. 6135941  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Yue, Henry  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Baughn, Mariah R.  
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/049,672A  
; FILING DATE: HEREWITH  
; CLASSIFICATION: 536







[illegible]

## RESULT 9

```

US/09-152-060-29
; Sequence 29, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003PL/US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29

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; LENGTH: 879  
 ; TYPE: DNA  
 ; ORGANISM: H  
 US-09-152-060-2

Query Match 61.6%; Score 434; DB 4; Length 879;  
Best Local Similarity 81.1%; Pred. NO. 4.le-111;  
Matches 519; Conservative 0; Mismatches 115; Indels

Qy	70	CTGACTCAGCCACCCCTCGGTGTCAGTGTCCTCCAGCAGACGCGCCAGGATCACCTGTGGG	129
Db	79	CTGACTCAGCCCCCTCGGTGTCCAGGACTTGAGACAGACCGCCACACTCACTTCGACC	138
Qy	130	GGAGACAACAGTAGAAATG-----AATATGTCCACTGGTACCAGCAGAAGCCAGCGGG	183
Db	139	GGGAACAACAATGTTTGGGACCAAGGACAGCTTGGCTGCAGCAGCAACAGGGCCAC	198
Qy	184	GCCCTTATCTGGTCACTCTATGATGATAGTACCGGCCCTCAGGGATCCCTGAGCGATTC	243
Db	199	CCTCCCAAACCTCCTGTCTCAGAGTAATAAATACCGGCCCTCAGGGATCTCAGAGAGATTA	258
Qy	244	TCTGGCTCCAAATCAGGGAACACCGCCACCTGTGACCATCAACGGGGTCGAGCCCGGGAT	303
Db	259	TCTGCATCCAGGTGAGGAGCACATCTCTCTGACCATTATGGAGCTCAAGCCTGAGGAC	318
Qy	304	GAGGCTGACTATTACTGTCAAGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAGGA	363
Db	319	GAGGCTGACTATTACTGGCAGCATATGACAGAGCCTCGCAGTTTGGATGTTCCGGGA	378
Qy	364	GGGACCGGGTGACCGTCTTAGTTCAGCCCAAGGTCGCCCTCGGTCACTCTGTTCCGG	423
Db	379	GGGACCAAGCTGACCGTCTAGGTGAGCCCAAGGTCGCCCTCGGTCACTCTGTTCCCA	438
Qy	424	CCCTCCTCTGAGGAGCTTCAAGCCAAACAAGGCCACACTGGTGTCCTATAGTGACTTC	483
Db	439	CCCTCCTCTGAGGAGCTTCAAGCCAAACAAGGCCACACTGGTGTCCTATAGTGACTTC	498
Qy	484	TACCCGGGAGCCGTGACAGTGGCTTGGAAAGCAGATAGCAGCCCGTCAAGCGGGAGTG	543
Db	499	TACCCGGGAGCCGTGACAGTGGCTTGGAAAGCAGATAGCAGCCCGTCAAGCGGGAGTG	558
Qy	544	GAGACCAACACACCTTCCAAACAAGCAACAACAGTAGCGGGCCAGCAGCTTACCTGAC	603
Db	559	GAGACCAACACACCTTCCAAACAAGCAACAACAGTAGCGGGCCAGCAGCTTACCTGAC	618
Qy	604	CTGACGCTGACAGTGGAAAGTCCACAGAAGACTACAGTGCAGGTCAAGCATGAAGGG	663
Db	619	CTGACGCTGACAGTGGAAAGTCCACAGAAGACTACAGTGCAGGTCAAGCATGAAGGG	678
Qy	664	AGCACCGTGGAGAGACAGTGGCCCCCTTACAGAAATGTTTCAT	703
Db	679	AGCACCGTGGAGAGAGCGTGGCCCCCTTACAGAAATGTTTCAT	718

## RESULT TO

US-09-152-060-46/c.  
 ; Sequence 46, Application US/09152060  
 ; Patent No. 6448230  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: 28 Human Secreted Proteins  
 ; FILE REFERENCE: P2003P1.US  
 ; CURRENT APPLICATION NUMBER: US/09/152,060  
 ; CURRENT FILING DATE: 1998-09-11  
 ; EARLIER APPLICATION NUMBER: PCT/US98/04858  
 ; EARLIER FILING DATE: 1998-03-12  
 ; EARLIER APPLICATION NUMBER: 60/040,762  
 ; EARLIER FILING DATE: 1997-03-14  
 ; EARLIER APPLICATION NUMBER: 60/040,710  
 ; EARLIER FILING DATE: 1997-03-14  
 ; EARLIER APPLICATION NUMBER: 60/050,934  
 ; EARLIER FILING DATE: 1997-05-30  
 ; EARLIER APPLICATION NUMBER: 60/048,100



Db 185 TGCGTTGAGCTCTGGCTCAGTCTCTACTAGTAATACCCAGCTGGTACAGCAGACCCC 244  
QY 177 AGCGCGGGCCCTATATCTGCTCATCTATGATGATGACCGGCGCTTCAGGGATCCTCTGA 236  
Db 245 AGCCAGGCTCCACGACGCTCATATAGCGACAAGTGTTCCTCTGAGTCCCTGA 304  
QY 237 GCATTTCTTGCTTCCAAATCAGGGAACACCGCCCTGACCATCAACAGGGTTCAGGC 296  
Db 305 TCCTCTCTGCTTCCATCTCTGGGAACAAAGCGGCTCACCATCAGCGGGGCCAGGC 364  
QY 297 CGGGGATGAGCTGACTATTACTGTCAGGTGGGACAGGCTAGTATCATCCGCTCT 356  
Db 365 AGATGATGATCTGATTAATTATGT---GTCTATATAGGCGTAGTGGTCTTTGGGTGT 421  
QY 357 CGGAGGAGGACCGGGTGACCGCTCTAGGTACGCCCAAGGCTGCCCTCGGTCACTCT 416  
Db 422 CGCGGAGGACCAAGCTGTCCTCTAGTCTAGGTACGCCCAAGGCTGCCCTCGGTCACTCT 481  
QY 417 GTTCCCGCTCTCTGAGGAGCTTCAAGCAACAAAGGCCACACTGCTGTGTCTCTAAG 476  
Db 482 GTTCCCACTCTCTGAGGAGCTTCAAGCAACAAAGGCCACACTGCTGTGTCTCTAAG 541  
QY 477 TGACTTCTACCGGGAGCGGTGACAGTGGCTGGAGGCGAGATAGCAGCCCGTCAAGC 536  
Db 542 TGACTTCTACCGGGAGCGGTGACAGTGGCTGGAGGCGAGATAGCAGCCCGTCAAGC 601  
QY 537 GCGAGTGGAGACCAACACACCTTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCTA 596  
Db 602 GCGAGTGGAGACCAACACACCTTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCTA 661  
QY 597 CTTGAGCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTTACAGCTGCGAGTCAAGCA 656  
Db 662 CTTGAGCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTTACAGCTGCGAGTCAAGCA 721  
QY 657 TGAAGGAGCACCGTGGAGAGACAGTGGCGCTTACAGATGTTTAT 703  
Db 722 TGAAGGAGCACCGTGGAGAGACAGTGGCGCTTACAGATGTTTAT 768

## RESULT 12

US-08-793-450-5  
; Sequence 5, Application US/08793450  
; Patent No. 6312690  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: MARGARITE, CHRISTEL  
; APPLICANT: KACZOREK, MICHEL  
; APPLICANT: CHABIRI, HASSAN  
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,450  
; FILING DATE: 03-MAR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94/10566  
; FILING DATE: 02-SEP-1994  
; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 716 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..716  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 1..57  
; NAME/KEY: mat\_peptide  
; LOCATION: 58..716  
; OTHER INFORMATION: /product= "IMMUNOGLOBIN, LIGHT"  
; OTHER INFORMATION: CHAIN"  
; US-08-793-450-5

Query Match 57.8%; Score 407.4; DB 4; Length 716;

Best Local Similarity 78.0%; Pred. No. 8.9e-104;

Matches 536; Conservative 0; Mismatches 106; Indels 45; Gaps 2;

QY 47 CAGGTGTCAGATGTGCTATGAATGACTCAGCCACCTCGGTGTGTCAGTGTCCCAAGGAC 106  
Db 44 CAGGTGTCCACTCCGACATCGAGTCACTCAGGACCTCTGTGTCTGTGGCTTGGGAC 103  
QY 107 AGACGCCAGGATCACTGTGGGGAGACAAAGTAGAATATATGTCCACTGCTTACC 166  
Db 104 AGACAGTCAGGATCACATCCAAAGGAGACAGCTCAGAACCTTATTGCAAGTGTGTACC 163  
QY 167 AGCAGAAAGCAGCGCGGGCCCTTATCTGTCTATCTATGATGATGACCGGCGCTCAG 226  
Db 164 AGCAGAAAGCAGGACAGGACCTGTACTTGTCTATGTTAAACACACCGGCGCTCAG 223  
QY 227 GGATCCCTGAGCGATTCTCTGGCTCCAAATCAGGGAAACACCGCCACCTGACCATCAACG 286  
Db 224 GGATCCAGACCGATTCTCTGGCTCCAGCTCAGGAAACACAGCTTCTTGTGACCATCACTG 283  
QY 287 GGTTCGAGCGCGGGATGAGGCTGACTATTACTGTCTAGGTGTGGGACAGGCTAGTGATC 346  
Db 284 GGGCTCAGCGGGAAGATAGGCTGACTATTCTGTAA-----CAGCGGTG 328  
QY 347 ATCCGGTCTTCGAGGAGGAGGACCGGGTGCACCGTCTCTAGGTACGCCCAAGGCTGCCCT 406  
Db 329 GGAAGTGTTCGCGGAGGAGGACCAAGTCACTGCTCTAGGTGAGCCCAAGGCTGCCCT 388  
QY 407 CGGTCACTCTGTTCGCGCTCC-----TCTGAGG 436  
Db 389 CGGTCACTCTGTTCGCGCTCCCTCCTCAGGAGCTTCAAGCAACAAAGGCCACACTCGAGG 448  
QY 437 AGCTTCAAGCCCAACAGGCGCACACTGCTGTGTCTATAGTACTTCTACCCGGGAGCCG 496  
Db 449 AGCTTCAAGCCCAACAGGCGCACACTGCTGTGTCTATAGTACTTCTACCCGGGAGCTG 508  
QY 497 TGACAGTGGCTTGAAGGAGGAGATAGCAGCCCGTCAAGCGGAGTGGAGACCAACACAC 556  
Db 509 TGACATTGGCTTGAAGGAGGAGATGGCAGGCCCGTCAAGCGGAGTGGAGACCAACAAAC 568  
QY 557 CCTCCAAACAAAGCAACAAAGTAGTACCGGCCAGCAGCTACCTGAGCCTTGAGCCTGAGC 616  
Db 569 CCTCCAAACAGAGCAACAAAGTAGTACCGGCCAGCAGCTACCTGAGCCTTGAGCCTGAGC 628  
QY 617 AGTGGAGTCCACAGAGCTACAGTGCAGGTGCGAGGTACGATGAGGAGGACCGTGGAGA 676  
Db 629 AGTGGAGTCCACAGAGCTACAGTGCAGGTGCGAGGTACGATGAGGAGGAGCACTGACAGA 688

QY 677 AGACAGTGGCCCTACAGATGTTTCAT 703  
|||||  
Db 689 AGACGTTGGCCCTCGCAGATGTTTCAT 715

## RESULT 13

US-09-404-879A-268/c  
; Sequence 268, Application US/09404879A  
; Patent No. 6468546  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: King, Gordon E.  
; APPLICANT: Algate, Paul A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C2  
; CURRENT APPLICATION NUMBER: US/09/404, 879A  
; CURRENT FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 393  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 268  
; LENGTH: 584  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; NAME/KEY: misc feature  
; LOCATION: (1)-(584)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-404-879A-268

Query Match 43.5%; Score 306.6; DB 4; Length 584;  
Best Local Similarity 85.0%; Pred. No. 6.8e-76;  
Matches 367; Conservative 0; Mismatches 57; Indels 8; Gaps 2;  
QY 215 ACCGGCCCTCAGGATCCCTGAGCGATTCTCTGGCTCCAAATCAGGG-----AACACCGC 269  
Db 449 AGCGGCCCTCAGGGTCCCTGATCGCTTNTCTGGCTTCCAAAGTCTTGGCAAAACACGGGCC 390  
QY 270 CACCCTGACCATCAACGGGCTCGAGCGGGGATGAGGCTGACTATTACTGTGACGTTG 329  
Db 389 TCCTTTGACNGTCTCTGGGCTCCAGGCTGAGGATGAGGCTGATTACTTGCAGCTCATA 330  
QY 330 GGACAGGGCTAGTATCATCGGCTCTCGGAGAGGAGACCGGGTGACCCCTCTAGGTCA 389  
Db 329 TGCAGGCAACA---ACAATTGGTGTTTCGCGGAGGGACCAAGCTGACCGTCTTAGTCA 273  
QY 390 GCCCAAGGCTGCCCGCTCGGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAA 449  
Db 272 GCCCAAGGCTGCCCGCTCGGTCACTCTGTTCCCAACCCCTCTCTGAGGAGCTTCAAGCCAA 213  
QY 450 CAAGGCCACACTGGTGCTCTCATAGTGACTTCTACCGGGAGCCGTGACAGTGGCCTG 509  
Db 212 CAAGGCCACACTGGTGCTCTCATAGTGACTTCTACCGGGAGCCGTGACAGTGGCCTG 153  
QY 510 GAAGGCAGATAGCAGCCCGCTCAAGCGGGAGTGGAGACCAACACACCCCTCCAAACAAAG 569  
Db 152 GAAGGCAGATAGCAGCCCGCTCAAGCGGGAGTGGAGACCAACACACCCCTCCAAACAAAG 93  
QY 570 CAACAACAATAGCCGGCCAGCAGCTACTTGACCTGAGCCCTGAGCAGTGGAGTCCCA 629  
Db 92 CAACAACAATAGCCGGCCAGCAGCTACTTGACCTGAGCCCTGAGCAGTGGAGTCCCA 33  
QY 630 CAGAAGCTACAG 641  
Db 32 CAGAAGCTACAG 21

## RESULT 14

US-08-991-789A-241/c  
; Sequence 241, Application US/08991789A  
; Patent No. 6225054  
; GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.  
Smith, John M.  
Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF BREAST CANCER  
NUMBER OF SEQUENCES: 292  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed IP Law Group  
STREET: 701 Fifth Avenue, Suite 6300  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/991,789A  
FILING DATE: 11-Dec-1997  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E. R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 210121.419C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 241:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 771 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
SEQUENCE DESCRIPTION: SEQ ID NO: 241:  
US-08-991-789A-241

Query Match 38.8%; Score 273.2; DB 4; Length 771;  
Best Local Similarity 79.2%; Pred. No. 1.3e-66;  
Matches 336; Conservative 0; Mismatches 85; Indels 3; Gaps 1;  
QY 131 GAGACAACAGTAAATGAATATGTCCTGCTACAGAGAGCCAGCGGGCCCTA 190  
Db 430 GTGACGTTGGTGTATATAATGTTCTNTGTTACCAACAGCACCCAGCAAGCCCCCA 371  
QY 191 TACTGTCTATCTATGATGATGATGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCT 250  
Db 370 AATTCATGATTTATGAGTTCGGTAAATCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCT 311  
QY 251 CCAATTCAGGGAACACCGCCACCTGACCATCAACGGGGTTCAGGCGGGGATGAGGCTG 310  
Db 310 CCAAGTNTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTG 251  
QY 311 ACTATTACTGTCAAGTGTGGGACAGGCTAGTATCATCCGGTCTTCGAGGAGGAGCC 370  
Db 250 ATTATTACTG---CAGCTCATATACAAGCAGCAGCACTCTCGTGTTCGGGAGGAGCA 194  
QY 371 GGGTGACCGCTCTTAGTTCAGCCCAAGGCTGCCCGCTCGGTCACTCTGTTCGCGCCCTCT 430  
Db 193 AGCTGACCGCTCTTAGTTCAGCCCAAGGCTGCCCGCTCGGTCACTCTGTTCGCGCCCTCT 134  
QY 431 CTGAGAGCTTCAAGCCAAACAGGCCACACTGGTGTCTCTAATAGTGACTTCTACCCGG 490  
Db 133 CTGAGAGCTTCAAGCCAAACAGGCCACACTGGTGTCTCTAATAGTGACTTCTACCCGG 74  
QY 491 GAGCCGTGACAGTGGCCTCGAAGGAGGATAGCAGCCCGCTCAAGCGGGGAGTGGAGACCA 550  
Db 73 GAGCCGTGACAGTGGCCTCGAAGGAGGATAGCAGCCCGCTCAAGCGGGGAGTGGAGACCA 14





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